



EUROPEAN PATENT SPECIFICATION

(45) Date of publication and mention of the grant of the patent:
16.12.2015 Bulletin 2015/51

(51) Int Cl.:
C12N 15/82 ^(2006.01) **C07K 14/33** ^(2006.01)
C12P 19/04 ^(2006.01) **C12N 9/42** ^(2006.01)

(21) Application number: **10011330.7**

(22) Date of filing: **26.07.1998**

(54) **Transgenic plants of altered morphology and the isolated arabidopsis thaliana endo-1,4-β-glucanase gene, promoter and protein**

Transgene Pflanzen mit veränderter Morphologie und isoliertes Arabidopsis-thaliana-Endo-1,4-β-glukanase-Gen, -Promotor und Protein

Plantes transgéniques à morphologie modifiée et gène, promoteur et protéine de l'endo-1,4-β-glucanase isolés à partir d'arabidopsis thaliana

(84) Designated Contracting States:
AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE

(30) Priority: **27.07.1997 IL 12140497**
13.01.1998 US 6632
13.01.1998 US 6636

(43) Date of publication of application:
21.09.2011 Bulletin 2011/38

(62) Document number(s) of the earlier application(s) in accordance with Art. 76 EPC:
98935257.0 / 1 009 805

(73) Proprietor: **Yissum Research Development Company of the Hebrew University of Jerusalem Ltd.**
9139002 Jerusalem (IL)

(72) Inventors:
• **Shoseyov, Oded**
72910 Karme Josef (IL)
• **Shani, Ziv**
Mazkeret Batia
76804 (IL)
• **Shpiegl, Etai**
Megido (IL)

(74) Representative: **Vossius & Partner**
Patentanwälte Rechtsanwälte mbB
Siebertstrasse 3
81675 München (DE)

(56) References cited:
WO-A-96/01555 WO-A1-91/16426
US-A1- 2010 333 223

- **LASHBROOK CORALIE C ET AL: "Two divergent endo-beta-1,4-glucanase genes exhibit overlapping expression in ripening fruit and abscising flowers", PLANT CELL, vol. 6, no. 10, 1994, pages 1485-1493, XP002649426, ISSN: 1040-4651**
- **DATABASE UniProt [Online] 1 February 1997 (1997-02-01), "SubName: Full=Cellulase (Endo-beta-1,4-glucanase); EC=3.2.1.4;"**, XP002649427, retrieved from EBI accession no. UNIPROT: Q96547 Database accession no. Q96547 -& **DATABASE EM_PL [Online] 31 October 1996 (1996-10-31), CASADORO G.: "Capsicum annuum mRNA for endo-beta-1,4-glucanase, ccel3", XP002649431, Database accession no. X97189**
- **BRUMMELL DAVID A ET AL: "A membrane-anchored E-type endo-1,4-beta-glucanase is localized on Golgi and plasma membranes of higher plants", PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, vol. 94, no. 9, April 1997 (1997-04), pages 4794-4799, XP001167019, ISSN: 0027-8424**
- **TRAINOTTI LIVIO ET AL: "Characterization of ppEG1, a member of a multigene family which encodes endo-beta-1,4-glucanase in peach", PLANT MOLECULAR BIOLOGY, vol. 34, no. 5, 1 July 1997 (1997-07-01), pages 791-802, XP008039730, ISSN: 0167-4412**

Note: Within nine months of the publication of the mention of the grant of the European patent in the European Patent Bulletin, any person may give notice to the European Patent Office of opposition to that patent, in accordance with the Implementing Regulations. Notice of opposition shall not be deemed to have been filed until the opposition fee has been paid. (Art. 99(1) European Patent Convention).

- | | |
|--|--|
| <ul style="list-style-type: none">• SHANIZ ET AL: "Cloning and characterization of elongation specific endo-1,4-beta-glucanase (cel1) from Arabidopsis thaliana", PLANT MOLECULAR BIOLOGY, NIJHOFF PUBLISHERS, DORDRECHT, NL, vol. 6, no. 34, August 1997 (1997-08), pages 837-842, XP002076142, ISSN: 0167-4412 | <ul style="list-style-type: none">• PARK ET AL.: PLANT JOURNAL, vol. 33, 2003, pages 1099-1106,• HARTATI ET AL.: PLANT PHYSIOLOGY, vol. 147, 2008, pages 552-561, |
|--|--|

Description

[0001] The present application claims priority benefits of Israeli Application No. 121404, filed July 27, 1997, and is a Continuation-in-part of U.S. Patent Application Nos. 09/006,632 and 09/006,636 both filed January 13, 1998, the disclosures of all of which are incorporated herein by reference in their entireties.

1. FIELD OF THE INVENTION

[0002] The present invention relates to the embodiments as characterized in the claims. Generally, the invention relates to plants genetically engineered to display altered structure or morphology. The altered structure or morphology is associated, with greater biomass or faster growth rate. More particularly, the present invention relates to transgenic plants expressing a cell wall modulation gene construct that results in a transgenic plant having altered structure or morphology as defined in the claims. The cell wall modulation transgene is a gene encoding a cell wall modifying enzyme as defined in the claims. The invention further relates to transgenic plants having altered structure or morphology expressing a transgene encoding a novel isolated endo-1,4- β -glucanase. The invention also relates to transgenic plants containing a gene construct encoding a secretion signal peptide with a cell wall modulation protein or polypeptide controlled by a constitutive or tissue specific promoter. In one embodiment, the tissue specific promoter is a novel elongating tissue specific promoter of *Arabidopsis thaliana*, i.e., the cell promoter. The specification also describes a novel isolated endoglucanase gene, i.e., the *Arabidopsis thaliana* endo-1,4- β -glucanase gene (*cel1*), its promoter (*cel1* promoter) and its encoded polypeptide (Cel1) and recombinant vectors containing the *cel1* gene with or without a secretion signal peptide sequence and/or the cell promoter.

2. BACKGROUND OF THE INVENTION

2.1. PLANT ELONGATION AND GROWTH

[0003] The plant cell elongation mechanism is a fundamental process with primary importance in plant-tissue development. Cell elongation requires relaxation of the rigid primary cell wall (Carpita and Gibeaut, 1993, Plant J. 3:1-30; Cosgrove, 1993, Plant Physiol. 102:1-6; Pry, 1988, The Growing Plant Cell Wall Chemical and Metabolic Analysis, Lonoman Scientific & Technical, New York; Roberts, 1994, Curr. Opin. Cell Biol. 6:688-694). Several mechanisms for this relaxation have been suggested, including the activities of endo-xyloglucan transferase (Nishitani and Tominaga, 1992, J. Biol. Chem. 267:21058-21064), xyloglucan endotransglycosylase (Fry et al., 1992, Biochem. J. 282:821-828) and expansins (McQueen-Mason and Cosgrove, 1995, Plant Physiol. 107:87-100). Endo-1,4- β -glucanase (hereinafter,

EGase) has been suggested to play an important role in the elongation process (Shoseyov and Dekel-Reichenbach, 1992, Acta Hort. 329:225-227; Verma et al., 1975, J. Biol. Chem. 250:1019-1026).

[0004] Substantial evidence for the involvement of a 1,3-1,4- β -glucan-specific enzyme in cell elongation was found in monocotyledons (Hatfield and Nevins, 1987, Plant Physiol. 83:203-207; Hoson and Nevins, 1989, Plant Physiol. 90:1353-1358 1989; Inouhe and Nevins, 1991, Plant Physiol. 96:426-431). EGase has been implicated in xyloglucan degradation during vegetative growth and fruit ripening (Hayashi, 1989, Ann. Rev. Plant Physiol. 40:139-168; Hayashi et al., 1984, Plant Physiol. 25:605-610). The activity of this enzyme could affect the generation of oligosaccharins, signaling molecules that are involved, among other things, in plant development and cell elongation (see for review, Darvill et al., 1992, Glycobiology 2:181-198).

[0005] To date, most of the EGase genes isolated have been studied in relation to fruit ripening (Cass et al., 1990, Mol. Gen. Genet. 223:76-86; Fischer and Bennett, 1991, Ann. Rev. Plant Physiol. Plant Mol. Biol. 42:675-703; Lashbrook et al., 1994, Plant Cell 6:1485-1493; Tucker et al., 1987, Plant Mol. Biol. 9:197-203) and abscission zones (Kemmerer and Tucker, 1994, Plant Physiol. 104:557-562; Tucker and Milligan, 1991, Plant Physiol. 95:928-933; Tucker et al., 1988, Plant Physiol. 88:1257-1262).

[0006] More recently, Wu et al. (1996, Plant Physiol. 110:163-170) cloned the EGase gene from pea and showed its expression to be induced by auxin in elongating epicotyls.

[0007] Endogenous regulation of cell elongation appears to be dominated by cell wall mechanics. This process is a result of the interaction between internal turgor pressure and the mechanical strength of the cell wall (reviewed by Steer and Steer, 1989, New Phytol. 111:323-358). Unlike most plant cells, the growth of pollen tubes and root hairs is restricted to the tip zone (reviewed by Cresti and Tiezzi, 1992, "Pollen tube emission organization and tip growth," in Sexual Plant Reproduction, pp. 89-97, eds. Cresti and Tiezzi, Springer-Verlag, Berlin). The growing region of pollen tubes consists of two distinct layers when fully mature. The inner layer consists mostly of callose-related molecules and the outer layer contains pectin, xyloglucan (XG), cellulose (at low levels and poor crystallinity) and other polysaccharides (reviewed by Steer and Steer, 1989, New Phytol. 111:323-358).

[0008] Xyloglucans (XGs) are linear chains of β -(1-4)-D-glucan, but unlike cellulose, they possess numerous xylosyl units added at regular sites to the 0-6 position of the glucosyl units of the chain (reviewed by Carpita and Gibeaut, 1993, Plant J. 3:1-30). XG can be extracted by alkaline treatment and then bound again *in vitro* to cellulose (Hayashi et al., 1994, Plant Cell Physiol. 35:1199-1205).

[0009] XG is bound to cellulose microfibrils in the cell

walls of all dicotyledons and some monocotyledons (reviewed by Roberts, 1994, *Curr. Opin. Cell Biol.* 6:688-694). The XG bound to the cellulose microfibrils cross-links the cell-wall framework.

[0010] Plant-cell expansion, including elongation, requires the integration of local wall-loosening and the controlled deposition of new wall materials. Fry et al. (1992, *Biochem J.* 282:821-828) and Nishitani and Tominaga (1992, *J. Biol. Chem.* 267:21058-21064) purified xyloglucan endo-transglycosylase (XET) and endo-xyloglucan transferase (EXT), respectively. These two enzymes were shown to be responsible for the transfer of intermicrofibrillar XG from one segment to another XG molecule and thus, suggested to be wall loosening-enzymes.

[0011] However, McQueen-Mason et al. (1993, *Planta* 190:327-331) showed that XET activity did not correlate with *in vitro* cell wall extension in cucumber hypocotyls.

[0012] The effect of XG on growing tissues has been extensively investigated. XG oligosaccharides, produced by partial digestion with β -(1-4)-D-glucanase and referred to as "oligosaccharins", alter plant-cell growth (reviewed by Aldington and Fry, 1993, *Advances in Botanical Research* 19:1-101). One such oligosaccharin, XXFG (XG9), antagonizes the growth promotion induced in pea stem segments by the auxin 2,4-D at a concentration of about 1 nM (York et al., 1984, *Plant Physiol.* 75:295-297; McDougall and Fry, 1988, *Planta* 175:412-416). On the other hand, at high concentrations (e.g., 100 μ M) oligosaccharins promote the elongation of etiolated pea stem segments (McDougall and Fry, 1990, *Plant Physiol.* 93:1042-1048). The mode of action of oligosaccharins is still unknown.

[0013] Another type of cell wall-loosening protein, termed "expansin", was isolated by McQueen-Mason et al. (1992, *The Plant Cell* 4:1425-1433). Expansin does not exhibit hydrolytic activity with any of the cell-wall components. It binds at the interface between cellulose microfibrils and matrix polysaccharides in the cell wall, and is suggested to induce cell wall expansion by reversibly disrupting noncovalent bonds within this polymeric network (McQueen-Mason and Cosgrove, 1995, *Plant Physiol.* 107:87-100).

[0014] Some cellulose-binding organic substances alter cell growth and cellulose-microfibril assembly *in vivo*. Direct dyes, carboxymethyl cellulose (CMC) and fluorescent brightening agents (FBAs, e.g., calcofluor white ST) prevent *Acetobacter xylinum* microfibril crystallization, thereby enhancing polymerization. These molecules bind to the polysaccharide chains immediately after their extrusion from the cell surface, preventing normal assembly of microfibrils and cell walls (Haigler, 1991, "Relationship between polymerization and crystallization in microfibril biogenesis," in *Biosynthesis and Biodegradation of Cellulose*, pp. 99-124, Haigler and Weimer eds., Marcel Dekker, Inc., New York). Haigler discusses dyes and fluorescent brightening agents that bind to cellulose alter cellulose microfibril assembly *in vivo*. Modifications in cell shape were observed when red alga (Waaland

and Waaland, 1975, *Planta* 126:127-138) and root tips (Hughes and McCully, 1975, *Stain Technology* 50:319-329) were grown in the presence of dyes. It is now evident that these molecules can bind to the cellulose chains immediately upon their extrusion from the cell surface of prokaryotes and eukaryotes (Haigler and Brown, 1979 *Science* 210:903-906; Benziman et al., 1980, *Proc. Natl. Acad. Sci. USA* 77:6678-6682; Haigler et al., 1980, *Science* 210:903-906; Brown et al., 1982, *Science* 218:1141-1142) and prevent crystal-structure formation (Haigler and Chanzy, 1988, *J. Ultrastruct. Mol. Struct. Res.* 98:299-311). In addition, the rate of cellulose polymerization was shown to increase in the presence of dye (Benziman et al., 1980). Crystallization was proposed to be the bottleneck in this coupled reaction and its prevention to result in accelerated cellulose synthase activity.

2.2. CELLULOSE BINDING PROTEINS AND DOMAINS

[0015] Many cellulase and hemicellulases (e.g., xylanases and mannanases) have the ability to associate with their substrates. These enzymes typically have a catalytic domain containing the active site for substrate hydrolysis and a carbohydrate-binding domain or cellulose-binding domain (herein generally designated "CBD") for binding the insoluble cellulosic or hemicellulosic matrices.

[0016] To date, more than one hundred and twenty cellulose-binding domains (CBDs) have been classified into ten families designated I-X (Tomme et al., 1995, "Cellulose-Binding Domains: Classification and Properties", in *ACS Symposium Series 618 Enzymatic Degradation and Insoluble Carbohydrates*, pp. 142-161, Saddler and Penner eds., American Chemical society, Washington, D.C.) (incorporated herein by reference). Most of the CBDs have been identified from cellulases and xylanases, but some are from other polysaccharides or from non-catalytic proteins. The CBDs identified thus far are from fungi, bacteria and slime molds.

[0017] The ten families of CBDs are as follows: family I CBDs are all from fungal β -1,4-glycanases; family II CBDs are found in bacterial hydrolases; family III CBDs are found in β -1,4-glucanases; family IV CBDs primarily have two conserved cysteine residues; family V is represented by a CBD from *Erwinia chrysanthemi*; family VI CBDs are primarily from xylanases and nearly all located at the C-terminal end of the protein; family VII is represented by the CBD of *Clostridium thermocellum*; family VIII is represented by the CBD of *Dictyostelium discoideum*; family IX CBDs are all known to be present as tandem repeats at the C-terminal end of thermostable xylanases; and family X is represented by xylanase E from *Pseudomonas fluorescens* spp. *cellulosa*. For a detailed description of the CBD families and individual members useful in the present invention, see Table II of Tomme et al.

[0018] Shoseyov and Doi (1990, *Proc. Natl. Acad. Sci.*

USA 87:2192-2195) isolated a unique cellulose-binding protein (CbpA) from the cellulase "complex" of the cellulolytic bacterium *Clostridium cellulovorans*. This major subunit of the cellulase complex was found to bind to cellulose, but had no hydrolytic activity, and was essential for the degradation of crystalline cellulose.

[0019] The *cbpA* gene has been cloned and sequenced (Shoseyov et al., 1992, Proc. Natl. Acad. Sci. USA 89:3483-3487). Using PCR primers flanking the cellulose-binding domain (herein, this specific CBD is designated "cbd") of CbpA, the latter was successfully cloned into an overexpression vector that enabled overproduction of the approximately 17 kDa cbd in *Escherichia coli*. The recombinant cbd exhibits very strong affinity to cellulose (U.S. Pat. No. 5,496,934; Goldstein et al., 1993, J. Bacteriol. 175:5762-5768; PCT International Publication WO 94/24158).

[0020] In recent years, several CBDs have been isolated from different sources. Most of these have been isolated from proteins that have separate catalytic, i.e., cellulase and cellulose binding domains, and only two have been isolated from proteins that have no apparent hydrolytic activity but possess cellulose-binding activity (Goldstein et al., 1993, J. Bacteriol. 175:5762-5768; Morag et al., 1995, Appl. Environ. Microbiol. 61:1980-1986).

2.3. *CLOSTRIDIUM CELLULOVORANS* CBD EFFECTS ON SEEDING AND POLLEN TUBE ELONGATION

[0021] The exogenous application of the cbd of *Clostridium cellulovorans* has been shown to modulate the elongation of pollen tubes and seedlings grown in culture. See PCT International Publication WO 94/24158 at pages 73-77.

[0022] The cbd of *C. cellulovorans* promoted pollen tube growth of peach pollen grains grown in liquid culture. Pollen grains exposed to 50 ug/ml of cbd produced pollen tubes almost twice size of pollen grains treated with bovine serum albumin (BSA) at 50 ug/ml.

[0023] Seeds of *Arabidopsis thaliana* germinated in distilled water in the presence of *C. cellulovorans* cbd responded differently to high versus low concentrations of cbd. High concentrations of cbd (1-100 ug/ml) dramatically reduced the root length. Low concentrations of cbd (1×10^{-6} to 1×10^{-4} ug/ml) promoted elongation of the roots whereas treatment with BSA had no effect. The effect on shoot length revealed a similar trend, but the differences between the treatments were not as dramatic as for the roots, and were not statistically different.

[0024] Cell walls of pollen tubes have been shown to contain exposed cellulose fibrils in the tip zone (reviewed by Steer and Steer, 1989, New Phytol. 111:323-358). Pollen tube elongation is known to be apical (reviewed by Cresti and Tiezzi, 1992, "Pollen tube emission, organization and tip growth", in Sexual Plant Reproduction, pp. 89-97, Cresti and Tiezzi eds., Springer-Verlag, Berlin).

Gold-immunolabelling of cbd in pollen tubes revealed that cbd was present primarily at the tip zone. Moreover, the lack of calcofluor staining in the tip zone of cbd-treated pollen tubes indicated the absence of a crystalline structure. See PCT International Publication WO 94/24158.

[0025] It has already been established that XG chains crosslink the cellulosic network in the cell wall (reviewed by Roberts, 1994, Curr. Opin. Cell Biol. 6:688-694). It is accepted that a prerequisite for cell elongation is a loosening of the cross-linked cellulose network, by either hydrolysis as demonstrated by Inouhe and Nevins (1991, Plant Physiol. 96:426-431), transglycosylation (Fry et al., 1992, Biochem. J. 282:821-828; Nishitani and Tominaga, 1992, J. Biol. Chem. 267:21058-21064), or expansins that interact with the XG-cellulose bond (McQueen-Mason et al., 1992, The Plant Cell 4:1425-1433). By *in vitro* competition assays it was shown that cbd competes with XG for binding to cellulose. Maximum cbd binding to cellulose is achieved after 1 hour (Goldstein et al. 1993, J. Bacteriol. 175:5762-5768), compared to XG binding to cellulose that is achieved only after 4 hour (Hayashi et al, 1987, Plant Physiol. 83:384-389). It is suggested that, during the elongation process, cellulose microfibrils become exposed and cbd competes with XG on binding to the exposed cellulose microfibril. It is therefore possible that this competition results in a temporary loosening of the cell wall and consequently enhanced elongation.

[0026] The inhibitory effect of cbd on root elongation can be explained by steric hindrance of the cellulose fibrils by excess amounts of cbd, which block access for enzymes or other proteins that modulate cell elongation via loosening, of the rigid cellulose-fibril network. This hypothesis is supported by Nevins, who prevented auxin-induced elongation with anti- β -D-glucan antibodies (Hosson and Nevins, 1989, Plant Physiol. 90:1353-1358) or with antibodies specific to cell wall glucanases (Inouhe and Nevins, 1991, Plant Physiol. 96:426-431).

[0027] The cbd of the CbpA protein of *C. cellulovorans* is a bacterial protein. Its mode of action in modulating cell wall elongation may be different from that of the natural process.

3. SUMMARY OF THE INVENTION

[0028] The present invention relates to the embodiments as characterized in the claims and provides transgenic plants which express a recombinant nucleic acid construct of a plant cell wall modulation protein or polypeptide so that the resulting plants have altered structure or morphology. The present invention particularly provides for altered structure or morphology by expressing a plant cell wall modulation protein or polypeptide that is a cell wall modifying enzyme as defined in the claims.

[0029] According to one embodiment of the present invention, achieving the desired plant of altered structural morphology entails expression of a plant cell wall modulation protein or peptide under the regulation of a suit-

able promoter as defined in the claims. In one mode of this embodiment, the promoter may be a plant promoter that is tissue- and/or developmental stage-specific. Suitable promoters include such as, an elongating tissue specific promoter (e.g., cell promoter), the chalcone synthase promoter (CHS), and the PATATIN promoter from potato. In an alternative mode of this embodiment, the promoter is constitutive and active in all plant tissues, substantially along its entire life cycle (e.g., the cauliflower mosaic virus (CaMV 35S) promoter). However, any combination of promoters and recombinant nucleic acids encoding cell wall modulation proteins and polypeptides as defined in the claims is also useful according to the invention.

[0030] Also according to the invention, the cell wall modulation recombinant nucleic acid may be secreted from the expressing plant cells which is achieved by having the cell wall modulation protein or polypeptide fused to any suitable secretion signal peptide.

[0031] The invention further provides seeds of transgenic plants wherein the seed has a plant cell wall modulation recombinant nucleic acid construct. The specification also encompasses progeny, clones, cell lines or cells of transgenic plants having a plant cell wall modulation recombinant nucleic acid, transgene, recombinant nucleic acid construct or transgene construct. Further, a novel endo- β -1,4-glucanase (EGase) gene (*cel1*) and protein (Cel1) from *Arabidopsis thaliana* is provided. Also provided is an elongating tissue specific promoter (*cel1* promoter) of the *A. thaliana* EGase gene or functional fragment thereof. Also, isolated nucleic acid molecules encoding proteins or polypeptides having the amino acid sequence of the *Arabidopsis cel1* of SEQ ID NO:4 or variants thereof are provided. In particular, an isolated nucleic acid molecule having the sequence of SEQ ID NO:2 is provided.

[0032] An isolated nucleic acid molecule comprising the genomic clone of the *Arabidopsis* endo-1,4- β -glucanase gene having the nucleotide sequence of SEQ ID NO:9 is also provided. Further, a polypeptide which includes an amino acid sequence corresponding to *Arabidopsis thaliana cel1* gene, as well as allelic and species variants, and functional naturally occurring and man-made variants thereof are provided. The present specification also provides derivatives or analogs of the *Arabidopsis* Cel1 polypeptide.

[0033] Further, the present specification provides for nucleotide vectors containing the above nucleotide sequences and host cells containing the recombinant nucleic acid vectors. Also, a polypeptide comprising the amino acid sequence of the *Arabidopsis* endo-1,4- β -glucanase (*cel1*) gene, allelic and species variants, and naturally occurring and man-made functional variants, derivatives and analogs thereof are provided. In addition, the proteins having endo-1,4- β -glucanase activity or the ability to bind cellulose or hemicellulose may have a non-naturally occurring amino acid sequence. A nucleic acid sequence encoding the latter may be derived from a ran-

dom display library, using, for example, cellulose as a screening agent.

[0034] The present specification further relates to recombinant nucleic acid vectors comprising a first nucleic acid sequence encoding a secretion signal peptide and second nucleic acid sequence encoding a cell wall modulation protein or polypeptide. The cell wall modulation proteins or polypeptides may be selected from cellulose binding proteins, cellulose binding domains and cell wall modifying enzymes.

[0035] The invention is based in part, on a number of unanticipated surprising discoveries. One is the discovery that expressing a cellulose binding protein or a cellulose binding domain (CBD) in transgenic plants results in transgenic plants having altered structural morphology. The other is the finding that expressing the *Arabidopsis thaliana* endo-1,4- β -glucanase in transgenic plants also results in plants having altered structural morphology. These findings together indicate that expressing a cell wall modulation transgene in plants results in plants having altered structure or morphology.

[0036] An object described herein is expression of any CBD in a transgenic plant to alter plant morphology, e.g. to stimulate or inhibit growth. It is an object to express any CBD, under the control, of the cell promoter, with the cell signal peptide to target the CBD to the cell wall thus resulting in tissue specific growth modulation.

[0037] The invention has utility in producing plants with altered structure or morphology as defined in the claims. Such altered structure or morphology provides plants that have an improved rate of growth and a greater biomass.

[0038] The *cel1* gene described herein has utility as a transgene encoding cell wall modulation protein or polypeptide in a transgenic plant to alter the structure or morphology. The *cel1* promoter described herein may be utilized as an elongating tissue specific plant promoter to express any protein, polypeptide or peptide of interest in a tissue specific manner in a transgenic plant. The *Arabidopsis thaliana* Cell protein described herein can be used in any biochemical applications. The Cell secretion peptide described herein may be utilized to facilitate the cellular secretion of any protein, polypeptide or peptide of interest.

3.1. DEFINITIONS

[0039] The term "altered structure or morphology" as used herein refers to any microscopic or macroscopic change in structure or morphology of a transgenic plant when compared to a progenitor plant cultivated under the same conditions. The altered structure or morphology can be associated, for example, with altered biomass, growth, yield, greater or less resistance to biodegradation, more or less digestible to ruminants, altered cellulose content, larger leaves/normal hypocotyls or smaller leaves/longer hypocotyls, starch production and/or content, modified fibers; time of blooming, etc. compared to a non-transgenic plant of the species.

[0040] The terms "protein", "polypeptide" and "peptide" are used interchangeably throughout the specification and claims. These terms also encompass glycosylated proteins, i.e., glycoproteins.

[0041] The term "cell wall modulation" as used herein refers to any alteration from a normal growth pattern of a plant. Therefore, according to the present invention, transgenic expression of a cell wall modulation protein or polypeptide as defined in the claim results in altered plant structure or morphology as defined in the claims.

[0042] The term "cellulose binding protein" refers to any protein, polypeptide or peptide including a glycoprotein, which specifically binds to cellulose or hemicellulose. The cellulose binding protein may or may not have cellulose or cellulolytic activity. The term "cellulose binding domain" (CBD) refers to any protein, polypeptide or peptide, including a glycoprotein, which is a region or portion of a larger protein, said region or portion which binds specifically to cellulose or hemicellulose. The cellulose binding domain (CBD) may be a part or portion of a cellulase, xylanase or other polysaccharidase, e.g. a chitinase, etc., a sugar binding protein such as maltose binding protein, etc., or a non-catalytic polysaccharide binding protein.

[0043] To date, more than one hundred and twenty cellulose-binding domains (CBDs) have been classified into at least thirteen families designated I-XIII (Tomme et al., 1995, "Cellulose-Binding Domains: Classification and Properties", in ACS-Symposium Series 618 Enzymatic Degradation and Insoluble Carbohydrates, pp. 142-161, Saddler and Penner eds., American Chemical Society, Washington, D.C.; Tomme et al., 1995, Adv. Microb. Physiol. 37:1; Smant et al., 1998, Proc. Natl. Acad. Sci. USA 95:4906-4911) (incorporated herein by reference). Any of the CBDs described in Tomme or any variants thereof, any other presently known CBDs or any new CBDs which may be identified can be used in the present invention. In addition, the CBD may be selected from a phage display peptide or peptidomimetic library, random or otherwise, using cellulose as a screening agent. (See Smith, 1985, Science 228:1315-1317 and Lam, 1991, Nature 354:82-84). Further, the CBD may be derived by mutation of a portion of a protein, polypeptide or peptide, including a glycoprotein, which binds to a polysaccharide other than cellulose (or hemicellulose), such as a chitinase, which specifically binds chitin, or a sugar binding protein such as maltose binding protein, rendering said portion capable of binding to cellulose. In any event, the CBD binds cellulose or hemicellulose.

4. BRIEF DESCRIPTION OF THE DRAWINGS

[0044]

FIG. 1 shows PCR products resolved on an agarose gel. Lane A: PCR products. The 260 bp fragment was used for further characterization. M: ladder DNA size marker of x 123 base pairs (bp) (Gibco BRL).

FIG. 2 is a schematic depiction of the *Arabidopsis thaliana cel1* genomic gene (SEQ ID NO:9) showing its DNA structure and restriction map. *EcoRI* - RI, *EcoRV* - R, *NcoI* - N, *Sall* - S, *SphI* - Sp, *XhoI* - X. The transcribed region is boxed. Exons - striped boxes. Introns - open boxes. 5' and 3' untranslated regions - shaded boxes. The three lines below the map indicate subclones used for *ExoIII* deletions. Numbers refer to nucleotides in SEQ ID NO:9. The extent of the 5' and 3' untranslated regions was not determined and is therefore indicated with question mark. FIG. 3 shows PCR amplification of a full-length reverse transcribed *A. thaliana cel1* cDNA (nucleotides 1-1479, SEQ ID NO:2). Lane A: the cDNA fragment. Lane B: control, PCR reaction performed on total mRNA which has not been pretreated with reverse transcriptase. M: 1 kb ladder DNA size marker (Gibco BRL).

FIG. 4 presents an optimal alignment of the deduced amino-acid sequences encoded by *A. thaliana cel1* (top, amino acids 2-490, SEQ ID NOs:3 and 4) and avocado *cel1* (bottom, amino acids 5-492, SEQ ID NO:8). Aligned cysteine residues are underlined. The potential glycosylation site (Asn-X-Ser/Thr) in Cell is boxed. The glycosyl hydrolase motif is both under- and abovelined.

FIG. 5 presents a Kyte-Doolittle hydropathy analysis of the *A. thaliana Cel1* protein (top), as compared to the avocado EGase (Cell, bottom).

FIG. 6 presents a northern blot analysis of cell. Lane 1: fully expanded leaf; Lane 2: the basal internode of the flowering stem; Lane 3: elongating zone in the flowering stem of a normal plant; Lane 4: elongating zone in the flowering stem of a dwarf plant (treated with uniconazole). The bottom lanes represent rRNA as internal standards.

FIGS. 7A-C present histological glucuronidase (GUS) staining of transgenic tobacco transformed with the *cel1* promoter region (nucleotides 5-1618, SEQ ID NO:1) fused to the *gus* reporter gene. FIG. 7A. The arrows are pointed to the blue stained elongating zones at the shoot and the root. FIG. 7B. enlarged shoot apex. FIG. 7C. enlarged root tip.

FIG. 8 shows the nucleic acid sequence of the *A. thaliana* promoter region of *cel1* (nucleotides 1-1770, SEQ ID NO: 1). The conserved promoter motifs TATA, CAT (x 2) and GC, and the translation initiator AUG codon are underlined.

FIG. 9 shows PCR amplification of genomic DNA of transgenic plants. The 500 bp band is indicative of the presence of a *cbd* transgene. Lanes 1 and 2: p35SC1.1 and p35SC1.2 transgenic plant clones. Lanes 3 and 4: pCC1.1 and pCC1.2 transgenic plant clones. Lanes 5 and 6: pBI101.1 and pBI101.2 transgenic plant clones. Lane 7: non transgenic plant. Lane 8: positive control - p35SC1 DNA. M: 1 kb ladder DNA size marker (Gibco BRL).

FIG. 10 shows (in negative) PCR amplification of re-

verse transcribed cDNA (RT-PCR) obtained from transgenic plants. The 500 bp band is indicative of the expression of a *cbd* transgene. Lane 1: positive control - p35SC1 DNA. Lane 2: negative control no reverse transcription. Lane 3: pBI101.1 transgenic plant clone. Lanes 4 and 5: p35SC1.1 (small phenotype) and p35SC1.2 (large phenotype) transgenic plant clones. M: 1 kb ladder (Gibco BRL).

FIGS. 11A-B are photographs of germination plates containing fourteen day old (A) tobacco plants derived from F₁ seeds obtained by selfing a pBI101 transgenic plant clone; and (B) tobacco plants derived from F₁ seeds obtained by selfing a p35SC1 transgenic plant clone.

FIGS. 12A-B are top and side photographs of eight week old F₁ p35SC1 tobacco plants demonstrating a large (left) and a small (right) phenotype. The plants were transferred from the germination plate after four weeks.

FIGS. 13A-B are photographs of germination plates containing four weeks vegetatively propagated F₁ p35SC1 transgenic plant clones of the large (A) and small (B) phenotypes.

FIGS. 14A-B are top and side photographs of ten week old vegetatively propagated F₁ p35SC1 tobacco plants demonstrating the large (right) and small (left) phenotypes.

FIG. 15A-F graphically shows a comparison of the biomass production of transgenic tobacco plants transformed with plasmid (p35SC1) compared to the control plants transformed with plasmid (pHI121) having either large phenotype (large leaves/normal hypocotyl) (FIGS. 15A-C) or small phenotype (small leaves/long hypocotyl) (FIGS. 15D-F). Measurements were taken of wet weight (FIGS. 15A and D), dry weight (FIGS. 15B and E) and leaf area (FIGS. 15C and F).

FIG. 16A-B graphically show a comparison of the biomass production of transgenic tobacco plants expressing *cbd* under the *cel1* promoter in plasmid pCC1 (pCC15.5) and wild type tobacco plants (wild). Measurements of weight (16A) and leaf area (16B) were taken.

FIG. 17 shows the expression of *cel1-gus* in Poplar. FIG. 18 shows the expression of *cell-gus* in a Poplar shoot.

FIG. 19 shows the expression of *cel1* promoter-*gus* in leaves transformed Poplar plants.

FIG. 20 shows the altered structural morphology of a transgenic Poplar plant expressing the *cbd* gene under control of the CaMV 35 promoter (right) as compared to the control untransformed Poplar plant (left).

FIG. 21 shows leaves from transgenic Poplar plants expressing the *cbd* gene under control of the CaMV 35S promoter (bottom) as compared to leaves of a control plant (top).

FIG. 22 shows roots from transgenic Poplar plant

expressing the *cbd* gene under control of the CaMV 35S promoter (right) compared to roots of a control plant (left).

FIG. 23 is a photograph of the root tip of a control poplar plant (40x magnification).

FIG. 24 is a photograph of the root tip of a transgenic poplar plant expressing the *cbd* gene under the CaMV 35S promoter (40x magnification).

FIG. 25 is a photograph of a calcofluor staining of a root from an untransformed control poplar plant (400x magnification).

FIG. 26 is a photograph of a calcofluor staining of a root from a transgenic poplar plant expressing the *cbd* gene under control of the CaMV 35S promoter (100x magnification).

FIG. 27 is a photograph of the calcofluor staining of a root hair from an untransformed control poplar plant (400x magnification).

FIG. 28 is a photograph of calcofluor staining of a root hair from a transgenic poplar plant expressing the *cbd* gene under the control of CaMV 35S promoter (400x magnification).

FIG. 29 is a photograph of a transgenic poplar plant expressing the *cel1* gene under control of the CaMV 35S promoter (right) and a control plant (left).

FIG. 30 is a photograph of a Western blot analysis of CEL1 protein in *Arabidopsis* tissues. Old leaf (OL), young leaf (YL), lower stem (LS), middle stem (MS), upper stem (US), old fruit/pod (OF), young fruit/pod (YF), flower (FL).

FIG. 31 is a graph depicting the effect of different concentrations of *cbd* on cellulose synthase activity as measured by the amount of glucose incorporation (nmol) in *Acetobacter xylinum*. The *cbd* concentrations listed were 0, 10, 100 and 50 mg/ml as compared to calcofluor and the control (BSA). Bars represent standard error.

FIGS. 32A-B are photographs of an electron microscopy examination of the effect of *cbd* on the type of cellulose ribbon produced by *Acetobacter xylinum* with *cbd*(A) or a control without *cbd*(B).

FIGS. 33A-D are photographs of light microscopy examination of the effect on the plant cell wall thickness of the expression of *cbd* (B and D) in poplar stems as compared to control plants (A and C).

FIGS. 34A-B are photographs of light microscopy examination of the effect of the expression of *cbd* in transgenic poplar roots (A) as compared to roots of control plants (B) as shown by calcofluor staining.

FIGS. 35A-B are photographs of light microscopy examination of the effect of the expression of *cbd* in root cells (A) as compared to root cells of control plants (B) as shown by CIZnI staining.

FIGS. 36A-B are photographs of light microscopy examination of the effect on starch granule accumulation of the expression by *cbd* in poplar stems (A) as compared to control plants (B) as shown by IKI staining. FIG. 36C is a photograph of light microscop-

py examination of IKI staining of starch granules in potato tubers provided for a comparison.

FIG. 37 is a graph depicting the effect of the expression of *cbd* gene under the control of the CaMV 35S promoter, or the *cel* promoter as compared to control poplar plants on the date of blooming of poplar plants. pBI101 (Clontech, Palo Alto, California) is the binary vector alone without an inserted recombinant nucleic acid coding region or transgene.

FIG. 38 is a graph depicting the effect on mean internode length of the expression of *cbd* in poplar stems of individual transgenic plants as compared to wild type plants.

FIG. 39 is a graph depicting the effect on the length of fiber cells from plants expressing *cel* (transgenic lines cell.5 and cell.8) as compared to wild type poplar plants.

FIG. 40 presents a Northern blot analysis of *cbd* gene expression. Lane 1: control wild type poplar plants; and lane 2: transgenic poplar plants expression a nucleic acid encoding CBD.

5. DETAILED DESCRIPTION OF THE INVENTION

[0045] The present invention is defined by the embodiments as characterized in the claims and provides transgenic plants which express a recombinant nucleic acid construct of a plant cell wall modulation protein or polypeptide so that the resulting plants have altered structure or morphology as defined in the claims. The present invention particularly provides for altered structure or morphology by expressing a plant cell wall modulation protein or polypeptide that is a cell wall modifying enzyme as defined in the claims.

[0046] Without intending to be limited to a particular mechanism, the inventors note that the targets for engineering are recombinant nucleic acids or genes encoding enzymes involved in the synthesis and/or rearrangement and/or degradation of cellulose in the plant cell wall as defined in the claims.

[0047] The proteins, polypeptides or enzymes can be expressed to engineer a plant with desirable properties. The engineering is accomplished by transforming plants with nucleic acid constructs described herein which may also comprise promoters and secretion signal peptides. The transformed plants or their progenies are screened for plants that express the desired protein, polypeptide or enzyme.

[0048] Engineered plants exhibiting the desired altered structure or morphology can be used in plant breeding or directly in agricultural production or industrial applications. Plants having one altered enzyme, protein or polypeptide can be crossed with other altered plants engineered with alterations in other growth modulation enzymes, proteins or polypeptides to produce lines with even further enhanced altered structural morphology characteristics compared to the parents or progenitor plants.

[0049] In another aspect, the present specification provides isolated nucleic acids encoding the *Arabidopsis thaliana* endo-1,4- β -glucanase (*cel1*), the *cel1* promoter and the Cel1 protein. The specification also provides isolated nucleic acid molecules comprising the genomic sequence of the *Arabidopsis thaliana cel* gene encoded by the nucleotide sequence of SEQ ID NO:9. The present specification further provides nucleic acid molecules encoding proteins or polypeptides having the amino acid sequence of the *A. thaliana Cel1* of SEQ ID No:4, as well as variants, derivatives or analogs thereof. The invention further provides nucleic acid vectors containing the described nucleic acid molecules and host cells containing the recombinant nucleic acid vectors. Uses of the *A. thaliana cel1* nucleic acid and Cell amino acid sequences are also provided.

[0050] Solely for ease of explanation, the description is divided into the following sections: (A) transgenic plants expressing a cell wall modulation protein; (B) methods for generating transgenic plants, including (i) preparation of nucleic acid constructs, including optimal expression nucleic acid constructs; (ii) transformation of plants and plant cells; (iii) selection and identification of transformed plants and plant cells; (C) identification and isolation of a novel endo-1,4- β -glucanase gene of *A. thaliana* (*cel1*) useful to express a cell wall modification protein in the transgenic plants and (D) applications of or uses for the transgenic plants and the novel *A. thaliana* endo-1,4- β -glucanase *cel1* gene, the cell signal sequence, the *cel1* promoter and Cell protein and polypeptide equivalents. The description of the novel *A. thaliana* endo-1,4- β -glucanase gene also includes a description of the protein encoded, the *cel* signal sequence and the *cel1* promoter, which itself is also useful as an elongating tissue specific promoter for the transgenic plants of the invention.

5.1. TRANSGENIC PLANTS

[0051] The present invention encompasses transgenic plants comprising a recombinant nucleic acid that directs the expression of a cell wall modulation protein or polypeptide, and the transgene plant exhibits altered structure or morphology compared with a progenitor plant which does not contain the recombinant nucleic acid, when the transgenic plant and the progenitor plant are cultivated under similar or equivalent growth conditions as defined in the claims. The cell wall modulation recombinant nucleic acid is a nucleic acid encoding cell wall modifying enzyme as defined in the claims. According to the specification the cell wall modulation recombinant nucleic acid or transgene is a nucleic acid encoding a cellulose binding domain. Any cellulose binding domain, as defined herein, can be used. For an illustrative, but in no way limiting example, a cellulose binding domain is obtainable from a bacterial, fungal or slime mold protein or polypeptide. For a more particular illustrative example, a cellulose binding domain is obtainable from *Clostridium*

cellulovorans, *Clostridium thermocellum* or *Cellulomonas fimi* (e.g., CenA, CenB, CenD, Cex). Examples of transgenic plants expressing a cellulose binding domain are presented *infra* herein in Sections 13, 15 and 18.

[0052] The cell wall modulation protein employed is an endo-1,4- β -glucanase (EGase). In a specific embodiment, the EGase is a novel EGase, i.e. Cel1. The EGase may also be obtained from tomato or avocado.

[0053] It is shown in the examples herein that transgenic plants expressing *Clostridium cellulovorans* CBD are growth modulated in strong correlation with their genotype (i.e., homozygote or heterozygote).

[0054] The recombinant nucleic acid may be selectively expressed in some tissues of the plant or at some developmental stages, or the recombinant nucleic acid may be expressed in substantially all plant tissues, substantially along its entire life cycle. However, any combinatorial expression mode is also applicable.

[0055] In another specific embodiment, the transgenic plant comprises a cell wall modulation protein or polypeptide which is an endo-1,4-8-glucanase. In a more specific embodiment, the EGase is obtainable from *Arabidopsis thaliana*. (See *infra* Section 5.3).

[0056] The present invention also encompasses transgenic plants having a recombinant nucleic acid construct comprising a recombinant nucleic acid encoding a cell wall modulation polypeptide operably linked to a promoter so that the cell wall modulation polypeptide is expressed in the transgenic plant, and the transgenic plant exhibits altered structure or morphology compared with a progenitor plant which does not contain the recombinant nucleic acid construct or gene construct when the transgenic plant and progenitor plant are cultivated under similar conditions as defined in the claims.

[0057] The promoter may be a constitutive plant promoter. The plant promoter may be the CaMV 35S promoter.

[0058] The promoter may be a tissue specific plant promoter. In a specific embodiment, the plant promoter is the elongating tissue specific cell promoter (see *infra* Section 5.3).

[0059] The plant promoter may be a development-specific promoter such as a seed specific, fruit specific, ripening specific, flowering specific promoter, etc.

[0060] In a preferred embodiment, the transgenic plant comprises the recombinant nucleic acid construct of the *ce1* promoter and *Ce1* encoding nucleic acid.

[0061] Also described herein is that the transgenic plant comprises the recombinant nucleic acid construct or gene construct of the *ce1* promoter and a CBD encoding nucleic acid.

[0062] In yet another preferred embodiment, the transgenic plant contains a recombinant nucleic acid construct or gene construct which further includes a secretion signal peptide, more particularly, the *ce1* secretion signal peptide.

[0063] The present invention also encompasses seeds of the transgenic plants as defined in the claims and de-

scribed above wherein the seed has the recombinant nucleic acid construct.

[0064] The present specification further encompasses the progeny, clones, cell lines or cells of the transgenic plants described above wherein said progeny, clone, cell line or cell has the recombinant nucleic acid, transgene, recombinant nucleic acid construct or gene construct.

5.2. GENERATING TRANSGENIC PLANTS

5.2.1. NUCLEIC ACID CONSTRUCTS

[0065] The properties of the nucleic acid sequences are varied as are the genetic structures of various potential host plant cells. This description of exemplary embodiments of the present invention includes a number of features which an artisan may recognize as not being absolutely essential, but clearly advantageous. These include methods of isolation, synthesis or construction of recombinant nucleic acid or gene constructs, the manipulations of the gene constructs to be introduced into plant cells, certain features of the gene constructs, and certain features of the vectors associated with the gene constructs.

[0066] Further, the gene constructs may be encoded on DNA or RNA molecules. According to the present invention, it is preferred that the desired, stable genotypic change of the target plant be effected through genomic integration of exogenously introduced nucleic acid construct(s), particularly recombinant DNA constructs. Nonetheless, according to the present invention, such genotypic changes can also be effected by the introduction of episomes (DNA or RNA) that can replicate autonomously and that are somatically and germinally stable. Where the introduced nucleic acid constructs comprise RNA, plant transformation or gene expression from such constructs may proceed through a DNA intermediate produced by reverse transcription.

[0067] The nucleic acid constructs described herein can be produced using methods well known to those skilled in the art. Artisans can refer to sources like Sambrook et al., 1989, Molecular cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, New York for teachings of recombinant DNA methods that can be used to isolate, characterize, and manipulate the components of the constructs as well as to build the constructs themselves. In some instances, where the nucleic acid sequence of a desired component is known, it may be advantageous to synthesize it rather than isolating it from a biological source. In such instances, an artisan can refer to teachings of references such as Caruthers et al., 1980, Nuc. Acids Res. Symp. Ser. 7:215-233, and Chow and Kempe, 1981, Nuc. Acids Res. 9:2807-2817. In other instances, the desired components may be advantageously produced by polymerase chain reaction (PCR) amplification. For PCR teachings, an artisan can refer to the references such as Gelfand, 1989, PCR Technology, Principles and Applications for DNA Amplification, H.A.

Erllich ed., Stockton Press, New York, 1988, Current Protocols In Molecular Biology, Vol. 2, Ch. 15, Ausubel et al. eds., John Wiley & Sons.

5.2.1.1. EXPRESSION CONSTRUCTS

[0068] In accord with the present invention, a transgenic plant with the ability to express a plant cell wall modulation polypeptide may be engineered by transforming a plant cell with a gene construct comprising a sequence encoding a plant cell wall modulation protein or polypeptide as defined in the claims. A plant promoter is operably associated with a sequence encoding the desired plant cell wall modulation protein or polypeptide. ("Operably associated" or "operably linked" is used herein to mean that transcription controlled by the "associated" or "operably linked" promoter produces a functional messenger RNA, whose translation produces the polypeptide.). The associated promoter may be a strong and non tissue- or developmental-specific plant promoter (e.g., a promoter that strongly expresses in many or all plant tissue types). Examples of such strong, "constitutive" promoters include, but are not limited to, the CaMV 35S promoter, the T-DNA mannopine synthetase promoter, and their various derivatives.

[0069] In another embodiment of the present invention, it may be advantageous to engineer a plant with a gene construct comprising a sequence encoding a plant cell wall modulation protein or polypeptide as defined in the claims operably associated with a tissue- or developmental-specific promoter, such as, but not limited to the *cel* promoter, the CHS promoter, the PATATIN promoter, etc. For example, where expression in elongating tissues and organs is desired, promoters such as the *cel* promoter may be used.

[0070] In yet another embodiment of the present invention, it may be advantageous to transform a plant with a gene construct comprising a sequence, encoding a plant cell wall modulation protein or polypeptide as defined in the claims operably linked to a modified or artificial promoter. Typically, such promoters, constructed by recombining structural elements of different promoters, have unique expression patterns and/or levels not found in natural promoters. See e.g., Salina et al., 1992, Plant Cell 4:1485-1493, for examples of artificial promoters constructed from combining cis-regulatory elements with a promoter core.

[0071] In yet an additional embodiment of the present invention, the expression of a cell wall modulation gene may be engineered by increasing the copy number of the gene encoding the desired protein or polypeptide. One approach to producing a plant cell with increased copies of the desired gene is to transform with nucleic acid constructs that contain multiple copies of the gene. Alternatively, a gene encoding the desired polypeptide can be placed in a nucleic acid construct containing an amplification-selectable marker (ASM) gene such as the glutamine synthetase (GS) or dihydrofolate reductase

gene. Cells transformed with such constructs are subjected to culturing regimes that select cell lines with increased copies of ASM gene. See Donn et al., 1984, J. Mol. Appl. Genet. 2:549-562, for a selection protocol used to isolate of a plant cell line containing amplified copies of the GS gene. Because the desired gene is closely linked to the ASM gene, cell lines that amplified the ASM gene would also likely to have amplified the gene encoding the desired growth modulation polypeptide. Also described is that the expression of a cell wall modulation protein or polypeptide may be engineered by transforming a plant cell with a nucleic acid construct encoding a regulatory gene that controls the expression of the endogenous gene or a transgene encoding the desired polypeptide, wherein the introduced regulatory gene is modified to allow for strong expression of the polypeptide in the desired tissues and/or developmental stages.

5.2.1.2. OTHER FEATURES OF RECOMBINANT NUCLEIC ACID CONSTRUCTS

[0072] The recombinant construct of the present invention may include a selectable marker for propagation of the construct. For example, a construct to be propagated in bacteria preferably contains an antibiotic resistance gene, such as one that confers resistance to kanamycin, tetracycline, streptomycin, or chloramphenicol. Suitable vectors for propagating the construct include plasmids, cosmids, bacteriophages or viruses, to name but a few.

[0073] In addition, the recombinant constructs may include plant-expressible selectable or screenable marker genes for isolating, identifying or tracking of plant cells transformed by these constructs. Selectable markers include, but are not limited to, genes that confer antibiotic resistances (e.g., resistance to kanamycin or hygromycin) or herbicide resistance (e.g., resistance to sulfonylurea, phosphinothricin, or glyphosate). Screenable markers include, but are not limited to, the genes encoding β -glucuronidase (Jefferson, 1987, Plant Molec Biol. Rep 5:387-405), luciferase (Ow et al., 1986, science 234:856-859), and the B and C1 gene products that regulate anthocyanin pigment production (Goff et al., 1990, EMBO J 9:2517-2522). Where the *Agrobacterium* system is utilized for transforming plants (see *intra*), the recombinant DNA constructs additionally comprise at least the right T-DNA border sequence flanking the DNA sequences to be transformed into plant cell. The sequences to be transferred in flanked by the right and left T-DNA border sequences. The proper design and construction of such T-DNA based transformation vectors are well known to those skilled in the art.

5.2.2. TRANSFORMATION OF PLANTS AND PLANT CELLS

[0074] As described herein, a desirable plant may be obtained by transforming a plant cell with a nucleic acid

construct described herein. In some instances, it may be desirable to engineer a plant or plant cell with several different gene constructs. Such engineering may be accomplished by transforming a plant or plant cell with all of the desired gene constructs simultaneously. Alternatively, the engineering may be carried out sequentially. That is, genetic engineering is accomplished by transforming with one gene construct, obtaining the desired transformant after selection and screening, transforming the transformant with a second gene construct, and so on. Each gene construct may be linked to a different selectable or screenable marker gene so as to facilitate the identification of plant transformants containing multiple gene inserts. Several different genes may be incorporated into one plant by crossing parental lines engineered for each gene.

[0075] *Agrobacterium* may be employed to introduce the gene construct into plants. Such transformation preferably uses binary *Agrobacterium* T-DNA vectors (Bevan, 1984, Nuc. Acid Res. 12:8711-8721), and the co-cultivation procedure (Horsch et al., 1985, Science 227:1229-1231). Generally, the *Agrobacterium* transformation system is used to engineer dicotyledonous plants (Bevan et al., 1982, Ann. Rev. Genet 16:357-384; Rogers et al., 1986, Methods Enzymol. 118:627-641). The *Agrobacterium* transformation system may also be used to transform, as well as transfer, DNA to monocotyledonous plants and plant cells. (see Hernalsteen et al., 1984, EMBO J 3:3039-3041; Hooykass-Van Slogteren et al., 1984, Nature 311:763-764; Grimsley et al., 1987, Nature 325:1677-179; Boulton et al., 1989, Plant Mol. Biol. 12:31-40.; and Gould et al., 1991, Plant Physiol. 95:426-434).

[0076] Various alternative methods for introducing recombinant nucleic acid constructs into plants and plant cells may also be utilized. These other methods are particularly useful where the target is a monocotyledonous plant or plant cell. Alternative gene transfer and transformation methods include, but are not limited to, protoplast transformation through calcium-, polyethylene glycol (PEG)- or electroporation-mediated uptake of naked DNA (see Paszkowski et al., 1984, EMBO J 3:2717-2722, Potrykus et al. 1985, Molec. Gen. Genet. 199:169-177; Fromm et al., 1985, Proc. Nat. Acad. Sci. USA 82:5824-5828; and Shimamoto, 1989, Nature 338:274-276) and electroporation of plant tissues (D'Halluin et al., 1992, Plant Cell 4:1495-1505). Additional methods for plant cell transformation include microinjection, silicon carbide mediated DNA uptake (Kaeppeler et al., 1990, Plant Cell Reporter 9:415-418), and microprojectile bombardment (see Klein et al., 1988, Proc. Nat. Acad. Sci. USA 85:4305-4309; and Gordon-Kamm et al., 1990, Plant Cell 2:603-618).

[0077] According to the present invention, a wide variety of plants and plant cell systems may be engineered for the desired physiological and agronomic characteristics described herein using the described nucleic acid constructs and the various transformation methods men-

tioned above. Target plants and plant cells for engineering include, but are not limited to, those monocotyledonous and dicotyledonous plants, such as crops including grain crops (e.g., wheat, maize, rice, millet, barley), fruit crops (e.g., tomato, apple, pear, strawberry, orange), forage crops (e.g., alfalfa), root vegetable crops (e.g., carrot, potato, sugar beets, yam), leafy vegetable crops (e.g., lettuce, spinach); flowering plants (e.g., petunia, rose, chrysanthemum), conifers and pine trees (e.g., pine fir, spruce); plants used in phytoremediation (e.g., heavy metal accumulating plants); oil crops (e.g., sunflower, rape seed) and plants used for experimental purposes (e.g., *Arabidopsis*).

5.2.3. SELECTION AND IDENTIFICATION OF TRANSFORMED PLANTS AND PLANT CELLS

[0078] Desired plants may be obtained by engineering one or more of the disclosed gene constructs into a variety of plant cell types, including but not limited to, protoplasts, tissue culture cells, tissue and organ explants, pollens, embryos as well as whole plants. The engineered plant material can be selected or screened for transformants (those that have incorporated or integrated the introduced gene construct(s)) following the approaches and methods described below. An isolated transformant may then be regenerated into a plant. Alternatively, the engineered plant material may be regenerated into a plant or plantlet before subjecting the derived plant or plantlet to selection or screening for the marker gene traits. Procedures for regenerating plants from plant cells, tissues or organs, either before or after selecting or screening for marker gene(s), are well known to those skilled in the art.

[0079] A transformed plant cell, callus, tissue or plant may be identified and isolated by selecting or screening the engineered plant material for traits encoded by the marker genes present on the transforming DNA. For instance, selection may be performed by growing the engineered plant material on media containing inhibitory amount of the antibiotic or herbicide to which the transforming gene construct confers resistance. Further, transformed plants and plant cells may also be identified by screening for the activities of any visible marker genes (e.g., the β -glucuronidase, luciferase, B or C1 genes) that may be present on the recombinant nucleic acid constructs of the present invention. Such selection and screening methodologies are well known to those skilled in the art.

[0080] Physical and biochemical methods also may be used to identify plant or plant cell transformants containing the gene constructs of the present invention. These methods include but are not limited to: 1) Southern analysis or PCR amplification for detecting and determining the structure of the recombinant DNA insert; 2) Northern blot, S1 RNase protection, primer-extension or reverse transcriptase-PCR amplification for detecting and examining RNA transcripts of the gene constructs; 3) enzy-

matic assays for detecting enzyme or ribozyme activity, where such gene products are encoded by the gene construct; 4) protein gel electrophoresis, Western blot techniques, immunoprecipitation, or enzyme-linked immunoassays, where the gene construct products are proteins. Additional techniques, such as *in situ* hybridization, enzyme staining, and immunostaining, also may be used to detect the presence or expression of the recombinant construct in specific plant organs and tissues. The methods for doing all these assays are well known to those skilled in the art.

5.3. *ARABIDOPSIS THALIANA* ENDO-1,4- β -GLUCANASE

5.3.1. *cel1* GENE, PROMOTER AND RECOMBINANT VECTORS

[0081] In another aspect, the present specification provides novel isolated nucleic acid molecules containing the nucleotide sequence encoding an endo-1,4- β -glucanase (Cel1) polypeptide of *Arabidopsis thaliana*. The polypeptide can have the amino acid sequence of SEQ ID NO:4.

[0082] The isolated nucleic acid molecule can have the nucleotide sequence of SEQ ID NO:2.

[0083] The isolated nucleic acid molecule encoding a polypeptide having the amino acid sequence of SEQ ID NO: 4 may be a variant such as an allelic variant, a species variant, a naturally occurring variant, a man-made or induced variant. The nucleic acid molecule may also encode derivatives or analogs of the polypeptide of SEQ ID NO:4.

[0084] As illustrated in the examples, *infra*, the isolation of the *cel1* gene was effected by PCR amplification of a 260 bp fragment using degenerate primers designed according to conserved amino-acid sequences in avocado and tomato EGases, which was thereafter used to screen an *A. thaliana* genomic library.

[0085] A 7.5 kb *SalI* fragment (SEQ ID NO:9) hybridizing with the 260 bp PCR fragment was isolated and analyzed. It was found that the *A. thaliana cel1* gene includes seven exons intercepted by six introns.

[0086] The present specification also provides an isolated nucleic acid molecule having the nucleotide sequence of SEQ ID NO:9 which is the *Arabidopsis thaliana* genomic clone of endo-1,4- β -glucanase.

[0087] Utilizing the nucleic acid sequence of the exons, RT-PCR was used to test for the presence of cell mRNA in elongating tissue and to isolate *cel1* cDNA which includes the open reading frame of *cel1*. A *cel1* 1.5 kb cDNA fragment was successfully cloned and sequenced (SEQ ID NO:2). The cDNA sequence perfectly matched the DNA sequence of the combined exons, as deduced from SEQ ID NO:9.

[0088] The 1476 bp open reading frame of cell was found to encode a 492 amino acid polypeptide (SEQ ID NO: 4) with a predicted molecular weight of 54 kDa.

[0089] As illustrated in the working examples, *infra*, northern blot analysis of *cel1* was carried out using a 768 bp *cel1* cDNA fragment as a probe. RNA transcripts were undetectable in fully expanded leaves, as well as at the basal internode of flowering stems. However-a strong transcript signal was detected in the elongating zone of flowering stems of normal plants.

[0090] Transgenic tobacco plants transformed with the putative *cel1* promoter region fused to the β -glucuronidase (GUS) reporter gene (*gus*), were tested for tissue-specific expression.

[0091] Significant GUS activity was observed in 16 seedlings that were generated from 8 independent transgenic plants. The staining was observed both in shoot and root elongating zones.

[0092] The *cel1* nucleic acid molecules described herein include (a) the DNA sequence shown in SEQ ID NO: 2; (b) any nucleotide sequence that encodes the amino acid sequence shown in SEQ ID NO:4; (c) any nucleotide sequence that hybridizes to the complement of the cDNA sequence shown in SEQ ID NO:2 and encodes a functionally equivalent product; (d) any nucleotide sequence that hybridizes to the complement of the DNA sequences that encode the amino acid sequence shown in SEQ ID NO:2 and encodes a functionally equivalent product; and (e) any nucleotide sequence encoding a plant protein containing the amino acid sequence of the endo-1,4- β -glucanase shown in SEQ ID NO:4. Functional equivalents of the *cel1* include naturally occurring plant *cel1* in other plant species, and mutant *cel1* whether naturally occurring or engineered. The specification also includes degenerate variants of sequences (a) through (e).

[0093] The specification also includes nucleic acid molecules, preferably DNA molecules, that hybridize to, and are therefore the complements of, the nucleotide sequences (a) through (e), in the preceding paragraph. Such hybridization conditions may be highly stringent or less highly stringent, as described below. In instances wherein the nucleic acid molecules are deoxyoligonucleotides ("oligos"), highly stringent conditions refers, *e.g.*, to washing in 6xSSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligos), 48°C (for 17-base oligos), 55°C (for 20-base oligos), and 60°C (for 23-base oligos).

[0094] The specification provides nucleic acid molecules having homologous sequences *e.g.*, nucleotide sequences sharing 60% or 70% or 80% or 90% or 95% homology or identity with the nucleotide sequence of SEQ ID NO:2 of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art or whose nucleic acid is capable of hybridizing to a Cel1 coding sequence, under high, moderately high or low stringency conditions.

[0095] By way of example and not limitation, procedures using conditions of low stringency are as follows (see also Shilo and Weinberg, 1981, Proc. Natl. Acad. Sci. USA 78:6789-6792): filters containing DNA are pre-

treated for 6 h at 40°C in a solution containing 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.1% PVP, 0.1% Ficoll, 1% BSA, and 500 µg/ml denatured salmon sperm DNA. Hybridizations are carried out in the same solution with the following modifications: 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 µg/ml salmon sperm DNA, 10% (wt/vol) dextran sulfate, and 5-20 X 10⁶ cpm ¹²P-labeled probe is used. Filters are incubated in Hybridization mixture for 18-20 h at 40°C, and then washed for 1.5 h at 55°C in a solution containing 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS. The wash solution is replaced with fresh solution and incubated an additional 1.5 h at 60°C. Filters are blotted dry and exposed for autoradiography. If necessary, filters are washed for a third time at 65-68°C and reexposed to film. Other conditions of low stringency which may be used are well known in the art.

[0096] By way of example and not limitation, procedures using conditions of high stringency are as follows: prehybridization of filters containing DNA is carried out for 8 h to overnight at 65°C in buffer composed of 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 µg/ml denatured salmon sperm DNA. Filters are hybridized for 48 h at 65°C in prehybridization mixture containing 100 µg/ml denatured salmon sperm DNA and 5-20 X 10⁶ cpm of ³²P-labeled probe. Washing of filters is done at 37°C for 1 h in a solution containing 2X SSC, 0.01% PVP, 0.01% Ficoll, and 0.01% BSA. This is followed by a wash in 0.1X SSC at 50°C for 45 min before autoradiography. Other conditions of high stringency which may be used are well known in the art.

[0097] By way of example and not limitation, procedures using conditions of moderately high stringency are as follows: filters containing DNA are pretreated for 6 hours to overnight at 55°C in buffer composed of 6X SSC, 5X Denhart's 0.5% SDS, 100 mg/mL salmon sperm DNA. Hybridizations are carried out in the same solution upon adding 5-20 X 10⁶ cpm of ¹²P-labeled probe and incubated 8-48 hours at 55°C. Washing of filters is done at 60°C in 1X SSC, 0.1% SDS, with two exchanges after 30 minutes. Other conditions for moderately high stringency screening are known in the art. For further guidance regarding hybridization conditions see, for example, Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, New York; and Ausubel et al., 1989, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, New York.

[0098] In addition to the plant *ce1* nucleotide sequences described above, full length plant *ce1* cDNA or gene sequences present in the same species and/or homologs of the *ce1* gene present in other plant species can be identified and readily isolated, without undue experimentation, by molecular biological techniques well known in the art. The identification of homologs of the *ce1* in related species can be useful for developing plant model systems for purposes of discovering plant cell agonists

or antagonists to modify cell in plants to alter the following processes in either a positive or negative way: larger or smaller altered plant morphology. Alternatively, such cDNA libraries, or genomic DNA libraries derived from the organism of interest can be screened by hybridization using the nucleotides described herein as hybridization or amplification probes. Furthermore, genes at other genetic loci within the genome that encode proteins which have extensive homology to one or more domains of the *ce1* gene product can also be identified via similar techniques. In the case of cDNA libraries, such screening techniques can identify clones derived from alternatively spliced transcripts in the same or different species.

[0099] Screening can be by filter hybridization, using duplicate filters. The labeled probe can contain at least 15-30 base pairs of the *ce1* nucleotide sequence, as shown in SEQ ID NO: 2. The hybridization washing conditions used should be of a lower stringency, as described above, when the cDNA library is derived from an organism different from the type of organism from which the labeled sequence was derived.

[0100] Alternatively, the labeled *ce1* nucleotide probe may be used to screen a genomic library derived from the organism of interest, again, using appropriately stringent conditions. The identification and characterization of plant genomic clones is helpful for use in transgenic plants for regulating plant structural morphology. For example, sequences derived from regions adjacent to the intron/exon boundaries of the plant gene can be used to design primers for use in amplification assays to detect mutations within the exons, introns, splice sites (e.g., splice acceptor and/or donor sites), etc.

[0101] Further, a *ce1* gene homolog may be isolated from nucleic acid of the organism of interest by performing PCR using two degenerate oligonucleotide primer pools designed on the basis of amino acid sequences within the plant *ce1* gene product disclosed herein. The template for the reaction may be cDNA obtained by reverse transcription of mRNA prepared from, for example, plant cell lines or tissue, known or suspected to express a *ce1* gene allele.

[0102] The PCR product may be subcloned and sequenced to ensure that the amplified sequences represent the sequences of a plant *ce1* gene. The PCR fragment may then be used to isolate a full length cDNA clone by a variety of methods. For example, the amplified fragment may be labeled and used to screen a cDNA library, such as a plant cDNA library. Alternatively, the labeled fragment may be used to isolate genomic clones via the screening of a genomic library.

[0103] PCR technology may also be utilized to isolate full length cDNA sequences. For example, RNA may be isolated, following standard procedures, from an appropriate cellular or tissue source (i.e., one known, or suspected, to express the plant *ce1* gene. A reverse transcription reaction may be performed on the RNA using an oligonucleotide primer specific for the most 5' end of the amplified fragment for the priming of first strand syn-

thesis. The resulting RNA/DNA hybrid may then be "tailed" with guanines using a standard terminal transferase reaction, the hybrid may be digested with RNAase H, and second strand synthesis may then be primed with a poly-C primer. Thus, cDNA sequences upstream of the amplified fragment may easily be isolated. For a review of cloning strategies which may be used, see e.g., Sambrook et al., 1989, supra.

[0104] The *cel1* gene sequences may additionally be used to isolate mutant *cel1* gene alleles. Such mutant alleles may be isolated from plant species either known or proposed to have a genotype which contributes to altered plant morphology. Additionally, such plant *cel1* gene sequences can be used to detect plant *cel1* gene regulatory (e.g., promoter or promoter/enhancer) defects which can affect plant growth.

[0105] A cDNA of a mutant plant *cel1* gene may be isolated, for example, by using PCR, a technique which is well known to those of skill in the art. In this case, the first cDNA strand may be synthesized by hybridizing an oligo-dT oligonucleotide to mRNA isolated from tissue known or suspected to be expressed in a plant species putatively carrying the mutant plant *cel1* allele, and by extending the new strand with reverse transcriptase. The second strand of the cDNA is then synthesized using an oligonucleotide that hybridizes specifically to the 5' end of the normal gene. Using these two primers, the product is then amplified via PCR, cloned into a suitable vector, and subjected to DNA sequence analysis through methods well known to those of skill in the art. By comparing the DNA sequence of the mutant plant *cel1* allele to that of the normal plant cell allele, the mutation(s) responsible for the loss or alteration of function of the mutant plant *cel1* gene product can be ascertained.

[0106] Alternatively, a genomic library can be constructed using DNA obtained from a plant species suspected of or known to carry the mutant plant *cel1* allele, or a cDNA library can be constructed using RNA from a tissue known, or suspected, to express the mutant plant *cel1* allele. The normal plant *cel1* gene or any suitable fragment thereof may then be labeled and used as a probe to identify the corresponding mutant plant *cel1* allele in such libraries. Clones containing the mutant plant *cel1* gene sequences may then be purified and subjected to sequence analysis according to methods well known to those of skill in the art.

[0107] Additionally, an expression library can be constructed utilizing cDNA synthesized from, for example, RNA isolated from a tissue known, or suspected, to express a mutant plant *cel1* allele in a plant species suspected of or known to carry such a mutant allele. In this manner, gene products made by the putatively mutant tissue may be expressed and screened using standard antibody screening techniques in conjunction with antibodies raised against the normal plant *cel1* gene product, as described, below, in Section 5.3. (For screening techniques, see, for example, Harlow, E. and Lane eds., 1988, *Antibodies: A Laboratory Manual*, Cold Spring Har-

bor Press, Cold Spring Harbor.) Additionally, screening can be accomplished by screening with labeled Cel1 fusion proteins. In cases where a plant *cel1* mutation results in an expressed gene product with altered function (e.g., as a result of a missense or a frameshift mutation), a polyclonal set of antibodies to plant *cel1* are likely to cross-react with the mutant plant *cel1* gene product. Library clones detected via their reaction with such labeled antibodies can be purified and subjected to sequence analysis according to methods well known to those of skill in the art.

[0108] The specification also describes nucleotide sequences that encode mutant plant *cel1*, peptide fragments of the plant Cel1, truncated plant Cel1, and plant Cel1 fusion proteins. These include, but are not limited to nucleotide sequences encoding mutant plant Cel1 described herein. Nucleotides encoding fusion proteins may include by are not limited to full length plant Cel1, truncated plant Cel1 or peptide fragments of plant Cel1 fused to an unrelated protein or peptide, such as for example, a secretion signal peptide.

[0109] The specification also describes Cel1 derivatives or analogues made by altering the *cel1* sequence by substitutions, additions or deletions that provide molecules with endo-1,4- β -glucanase activity. Thus, the Cel1 derivatives include polypeptides containing, as a primary amino acid sequence, all or part of the Cel1 amino acid sequence including altered sequences in which functionally equivalent amino acid residues are substituted for residues within the sequence resulting in a polypeptide which is functionally active. For example, one or more amino acid residues within the sequence can be substituted by another amino acid of a similar polarity which acts as a functional equivalent, resulting in a silent alteration. Conservative substitutions for an amino acid within the sequence may be selected from other members of the class to which the amino acid belongs. For example, the nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan and methionine. The polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine. The positively charged (basic) amino acids include arginine, lysine and histidine. The negatively charged (acidic) amino acids include aspartic acid and glutamic acid. Such Cel1 derivatives can be made either by chemical peptide synthesis or by recombinant production from nucleic acid encoding the Cel1 which nucleic acid has been mutated. Any technique for mutagenesis known in the art can be used, including, but not limited to, chemical mutagenesis, *in vitro* site-directed mutagenesis (Hutchinson et al., 1978, *J. Biol. Chem.* 253:6551), use of TAB® linkers (Pharmacia), PCR with mutation-containing primers, etc.

[0110] Furthermore, if desired, nonclassical amino acids or chemical amino acid analogues can be introduced as a substitution or addition into the Cel1 protein, derivative or analogue. Non-classical amino acids include, but are not limited to, the D-isomers of the common amino

acids, 2,4-diaminobutyric acid, α -amino isobutyric acid, 4-aminobutyric acid, Abu, 2-amino butyric acid, γ -Abu, ϵ -Ahx, 6-amino hexanoic acid, Aib, 2-amino isobutyric acid, 3-amino propionic acid, ornithine, norleucine, norvaline, hydroxyproline, sarcosine, citrulline, homocitrulline, cysteic acid, t-butylglycine, t-butylalanine, phenylglycine, cyclohexylalanine, β -alanine, fluoro-amino acids, designer amino acids such as β -methyl amino acids, C α -methyl amino acids, N α -methyl amino acids, and amino acid analogues in general. Furthermore, the amino acid can be D (dextrorotary) or L (levorotary).

[0111] The specification also describes to isolated nucleic acid molecules which comprise the nucleotide sequence of the *cel1* promoter.

[0112] The isolated nucleic acid molecule may comprise or consist of the nucleotide sequence of SEQ ID NO: 1 or functional fragments thereof.

[0113] The specification also describes (a) recombinant nucleic acid vectors that contain any of the foregoing plant *cel1* coding sequences and/or their complements (*i.e.*, antisense); (b) recombinant nucleic acid expression vectors that contain any of the foregoing *cel1* coding sequences operatively associated with a regulatory element that directs the expression of the coding sequences; and (c) genetically engineered host cells that contain any of the foregoing plant cell coding sequences operatively associated with a regulatory element that directs the expression of the coding sequences in the host cell. As used herein, regulatory elements include but are not limited to inducible and non-inducible promoters, enhancers, operators and other elements known to those skilled in the art that drive and regulate expression. Such regulatory elements include but are not limited to the promoters derived from the genome of plant cells (*e.g.*, heat shock promoters; the promoter for the small subunit of RUBISCO; the promoter for the chlorophyll a/b binding protein) or from plant viruses (*e.g.*, the 35S RNA promoter of CaMV; the coat protein promoter of tobacco mosaic virus (TMV), cytomegalovirus hCMV immediate early gene, the early or late promoters of SV40 adenovirus, the *lac* system, the *trp* system, the *TAC* system, the *TRC* system, the major operator and promoter regions of phage A, the control regions of fd coat protein, the promoter for 3-phosphoglycerate kinase, the promoters of acid phosphatase, and the promoters of the yeast α -mat factors).

[0114] The present specification also describes a recombinant nucleic acid vector comprising the nucleic acid molecule comprising (a) the nucleotide sequence encoding a protein or polypeptide having the amino acid sequence of SEQ ID NO:4; (b) variant nucleotide sequences of SEQ ID NO:4 which is an allelic variant, species variant, and naturally occurring or man-made functional variants thereof; (c) a nucleic acid molecule encoding derivatives or analogs of the Cel1 polypeptide of SEQ ID NO:4; or (d) the nucleotide sequence of SEQ ID NO: 2.

[0115] The specification also describes host cells containing the recombinant nucleic acid vectors described

above.

[0116] The present specification further describes recombinant nucleic acid vectors comprising a first nucleic acid sequence encoding a secretion signal peptide and a second nucleic acid sequence encoding a cell wall modulation polypeptide.

[0117] In another specific embodiment, the secretion signal peptide is from *cel1*, obtainable from *Arabidopsis thaliana*.

[0118] The recombinant nucleic acid vector may have a cell wall modulation protein polypeptide which is a cellulose binding domain as defined above herein.

5.3.2. Cel1 PROTEINS AND POLYPEPTIDES

[0119] The present specification encompasses polypeptides comprising an amino acid sequence corresponding to *Arabidopsis thaliana* endo-1,4- β -glucanase (Cel1) gene, allelic and species variants, and naturally occurring and man-made functional variants, and derivatives and analogs thereof.

[0120] The present specification provides a polypeptide having the amino acid sequence of SEQ ID NO:4.

[0121] Cel1 proteins, polypeptides and peptide fragments, mutated, truncated or deleted forms of the Cel1 and/or Cel1 fusion proteins can be prepared for use as cell wall modulating polypeptides.

[0122] The specification also encompasses proteins that are functionally equivalent to the Cel1 encoded by the nucleotide sequences described in Section 5.3.1, *supra*, as judged by any of a number of criteria, including but not limited to endo-1,4- β -glucanase activity. Such functionally equivalent Cel1 proteins include but are not limited to additions or substitutions of amino acid residues within the amino acid sequence encoded by the plant cell nucleotide sequences described, above, in Section 5.3.1, but which result in a silent change, thus producing a functionally equivalent gene product. Amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid.

[0123] While random mutations can be made to *cel1* DNA (using random mutagenesis techniques well known to those skilled in the art) and the resulting mutant *cel1* tested for activity, site-directed mutations of the *cel1* coding sequence can be engineered (using site-directed mutagenesis techniques well known to those skilled in the art) to generate mutant plant cells with increased function.

[0124] Other mutations to the *cel1* coding sequence

can be made to generate Cell proteins that are better suited for expression, scale up, etc. in the host cells chosen. For example, cysteine residues can be deleted or substituted with another amino acid in order to eliminate disulfide bridges; N-linked glycosylation sites can be altered or eliminated to achieve, for example, expression of a homogeneous product that is more easily recovered and purified from yeast hosts which are known to hyperglycosylate N-linked sites.

[0125] While the Cell polypeptides and peptides can be chemically synthesized (e.g., see Creighton, 1983, *Proteins: Structures and Molecular Principles*, W.H. Freeman & Co., New York), large polypeptides derived from the Cel1 and the full length Cel1 itself may advantageously be produced by recombinant DNA technology using techniques well known in the art for expressing nucleic acid containing plant Cel1 gene sequences and/or coding sequences. Such methods can be used to construct expression vectors containing the *cel1* nucleotide sequences described in Section 5.1 and appropriate transcriptional and translational control signals. These methods include, for example, *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination. See, for example, the techniques described in Sambrook et al., 1989, *supra*, and Ausubel et al., 1989, *supra*. Alternatively, RNA capable of encoding *cel1* nucleotide sequences may be chemically synthesized using, for example, synthesizers. See, for example, the techniques described in *Oligonucleotide Synthesis*, 1984, Gait, M.J. ed., IRL Press, Oxford, which is incorporated by reference herein in its entirety.

[0126] Also included within the scope of the specification are Cel1 proteins, derivatives, and analogues which are differentially modified during or after synthesis, e.g., by biotinylation, benzylation, glycosylation, acetylation, phosphorylation, amidation, pegylation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to an antibody molecule or other cellular ligand, etc. The MDC proteins, derivatives, or analogues can be acetylated at the N-terminus and/or amidated at the C-terminus. Any of numerous chemical modifications may be carried out by known techniques, including, but not limited to, acetylation, formylation, oxidation, reduction, metabolic synthesis in the presence of tunicamycin, etc. These modifications may serve to increase the stability, bioavailability and/or inhibitory action of the peptides of the invention.

[0127] Any of the Cell proteins, derivatives or analogues described above may, additionally, have a non-peptide macromolecular carrier group covalently attached to its amino and/or carboxy termini. Such macromolecular carrier groups may include, for example, lipid-fatty acid conjugates or carbohydrates.

[0128] Endo-1,4- β -glucanase activity and/or the ability to bind cellulose of the Cel1 variants or derivatives (including fragments and chimeric proteins) or analogues thereof, for use in transgenic plants can be demonstrated by any of the methods disclosed in Sections 5.4 and 6

infra or known to one skilled in the art.

[0129] A variety of host-expression vector systems may be utilized to express the plant *cel1* nucleotide sequences of the invention.

[0130] Methods which are well known to those skilled in the art can be used to construct expression vectors containing the plant *cel1* coding sequence and appropriate transcriptional/translational control signals. These methods include *in vitro* recombinant DNA techniques, synthetic techniques and *in vivo* recombination/genetic recombination. See, for example, the techniques described in Maniatis et al., 1989, *Molecular Cloning A Laboratory Manual*, Cold Spring Harbor Laboratory, New York and Ausubel et al., 1989, *Current Protocols in Molecular Biology*, Greene Publishing Associates and Wiley Interscience, New York.

[0131] A variety of host-expression vector systems may be utilized to express the cell coding sequence. These include but are not limited to microorganisms such as bacteria transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors containing the plant GluR coding sequence; yeast transformed with recombinant yeast expression vectors containing the plant GluR coding sequence; insect cell systems infected with recombinant virus expression vectors (e.g., baculovirus) containing the *cel1* coding sequence; plant cell systems infected with recombinant virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, THV) or transformed with recombinant plasmid expression vectors (e.g., Ti plasmid) containing the *cel1* coding sequence; or animal cell systems infected with recombinant virus expression vectors (e.g., adenovirus, vaccinia virus) including cell lines engineered to contain multiple copies of the *cel1* either stably amplified (CHO/dhfr) or unstably amplified in double-minute chromosomes (e.g., murine cell lines).

[0132] The expression elements of these systems vary in their strength and specificities. Depending on the host/vector system utilized, any of a number of suitable transcription and translation elements, including constitutive and inducible promoters, may be used in the expression vector. For example, when cloning in bacterial systems, inducible promoters such as pL of bacteriophage X, plac, ptrp, ptac (ptrp-lac hybrid promoter) and the like may be used; when cloning in insect cell systems, promoters such as the baculovirus polyhedrin promoter may be used; when cloning in plant cell systems, promoters derived from the genome of plant cells (e.g., the *cel1* promoter, heat shock promoters; the promoter for the small subunit of RUBISCO; the promoter for the chlorophyll a/b binding protein) or from plant viruses (e.g., the 35S RNA promoter of CaMV; the coat protein promoter of TMV) may be used; when cloning in mammalian cell systems, promoters derived from the genome of mammalian cells (e.g., metallothionein promoter) or from mammalian viruses (e.g., the adenovirus late promoter; the vaccinia virus 7.5K promoter) may be used; when generating cell lines that contain multiple copies of the

ce1 DNA SV40-, BPV- and EBV-based vectors may be used with an appropriate selectable marker.

[0133] In bacterial systems a number of expression vectors may be advantageously selected depending upon the use intended for the *Ce1* expressed. For example, when large quantities of *Ce1* are to be produced for the generation of antibodies or to screen peptide libraries, vectors which direct the expression of high levels of fusion protein products that are readily purified may be desirable. Such vectors include but are not limited to the *E. coli* expression vector pUR278 (Ruther et al., 1983, EMBO J. 2:1791), in which the *ce1* coding sequence may be ligated into the vector in frame with the lac Z coding region so that a hybrid *Ce1* lac Z protein is produced; *E. coli* expression vector pET3d obtained from Novagen (Madison, Wisconsin) as we have already successfully prepared and used to purify antibodies from rabbits; pIN vectors (Inouye & Inouye, 1985, Nucleic acids Res. 13:3101-3109; Van Heeke & Schuster, 1989, J. Biol. Chem. 264:5503-5509); and the like.

[0134] In yeast, a number of vectors containing constitutive or inducible promoters may be used. For a review see, Current Protocols in Molecular Biology, Vol. 2, 1988, Ausubel et al. eds., Greene Publish. Assoc. & Wiley Interscience, Ch. 13; Grant et al., 1987, Expression and Secretion Vectors for Yeast, in Methods in Enzymology, Wu & Grossman eds., 1987, Acad. Press, N.Y., Vol. 153, pp. 516-544; Glover, 1986, DNA Cloning, Vol. II, IRL Press, Wash., D.C., Ch. 3; and Bitter, 1987, "heterologous Gene Expression in Yeast", Methods in Enzymology, Berger & Kimmel eds., Acad. Press, N.Y., Vol. 152, pp. 673-684; and The Molecular Biology of the Yeast *Saccharomyces*, 1982, Strathern et al. eds., Cold Spring Harbor Press, vols. I and II.

[0135] In cases where plant expression vectors are used, the expression of the *ce1* coding sequence may be driven by any of a number of promoters. For example, viral promoters such as the 35S RNA and 19S RNA promoters of CaMV (Brisson et al., 1984, Nature 310:511-514), or the coat protein promoter of TMV (Takamatsu et al., 1987, EMBO J. 6:307-311) may be used; alternatively, plant promoters such as the cell promoter or functional fragments thereof, the small subunit of RUBISCO (Coruzzi et al., 1984, EMBO J. 3:1671-1680; Broglie et al., 1984, Science 224:838-843); or heat shock promoters, e.g., soybean hsp17.5-E or hsp17.3-B (Gurley et al., 1986, Mol. Cell. Biol. 6:559-565) may be used. These constructs can be introduced into plant cells using Ti plasmids, Ri plasmids, plant virus vectors, direct DNA transformation, microinjection, electroporation, etc. For reviews of such techniques see, for example, Weissbach & Weissbach, 1988, Methods for Plant Molecular Biology, Academic Press, NY, Section VIII, pp. 421-463; and Grierson & Corey, 1988, Plant Molecular Biology, 2d Ed., Blackie, London, Ch. 7-9.

[0136] For long-term, high-yield production of recombinant proteins, stable expression is preferred. For example, cell lines which stably express the plant *Ce1* pro-

tein may be engineered. Rather than using expression vectors which contain viral origins of replication, host cells can be transformed with the *ce1* DNA controlled by appropriate expression control elements (e.g., promoter, enhancer, sequences, transcription terminators, polyadenylation sites, etc.), and a selectable marker. Following the introduction of foreign DNA, engineered cells may be allowed to grow for 1-2 days in an enriched media, and then are switched to a selective media. The selectable marker in the recombinant plasmid confers resistance to the selection and allows cells to stably integrate the plasmid into their chromosomes and grow to form foci which in turn can be cloned and expanded into cell lines.

[0137] A number of selection systems may be used, including but not limited to the herpes simplex virus thymidine kinase (Wigler, et al., 1977, Cell 11:223), hypoxanthine-guanine phosphoribosyltransferase (Szybalska & Szybalski, 1962, Proc. Natl. Acad. Sci. USA 48:2026), and adenine phosphoribosyltransferase (Lowy et al., 1980, Cell 22:817) genes can be employed in tk⁻, hgp^rt or apr^t cells, respectively. Also, antimetabolite resistance can be used as the basis of selection for dhfr, which confers resistance to methotrexate (Wigler et al., 1980, Natl. Acad. Sci. USA 77:3567; O'Hare et al., 1981, Proc. Natl. Acad. Sci. USA 78:1527); gpt, which confers resistance to mycophenolic acid (Mulligan & Berg, 1981, Proc. Natl. Acad. Sci. USA 78:2072); neo, which confers resistance to the aminoglycoside G-418 (Colberre-Garapin et al., 1981, J. Mol. Biol. 150:1); and hyg^r, which confers resistance to hygromycin genes (Santerre, et al., 1984, Gene 30:147). Recently, additional selectable genes have been described, namely trpB, which allows cells to utilize indole in place of tryptophan; hisD, which allows cells to utilize histinol in place of histidine (Hartman & Mulligan, 1988, Proc. Natl. Acad. Sci. USA 85:8047); and ODC (ornithine decarboxylase) which confers resistance to the ornithine decarboxylase inhibitor, 2-(difluoromethyl)-DL-ornithine, DFMO (McConlogue L., 1987, in Current Communications in Molecular Biology, Cold Spring Harbor Laboratory ed.). The invention also encompasses (a) DNA vectors that contain any of the foregoing coding sequences and/or their complements (i.e., antisense); (b) DNA expression vectors that contain any of the foregoing coding sequences operatively associated with a regulatory element that directs the expression of the coding sequences; and (c) genetically engineered host cells and/or plants that contain any of the foregoing coding sequences operatively associated with a regulatory element that directs the expression of the coding sequences in the host cell. As used herein, regulatory elements include but are not limited to inducible and non-inducible promoters, enhancers, operators and other elements known to those skilled in the art that drive and regulate expression.

5.3.3. PREPARATION OF Cel1 PROTEINS, DERIVATIVES AND ANALOGUE

[0138] The endo-1,4-B-glucanase (Cel1), and derivatives or analogues thereof can be purified from biological tissue or cell culture, or produced by recombinant or synthetic techniques known in the art.

[0139] Native Cel1 preparations can be obtained from a variety of sources. Standard methods of protein purification may be used to isolate and purify, or partially purify, endo-1,4-β-glucanases from any source known to contain or produce the desired endo-1,4-β-glucanase (Cel1), e.g., Cel1 may be isolated from sources such as plant tissues. Such standard protein purification techniques include, but are not limited to, chromatography (e.g., ion exchange, affinity, gel filtration/molecular exclusion chromatography and reversed phase high performance liquid chromatography (RP-HPLC)), centrifugation, differential solubility, and electrophoresis (for a review of protein purification techniques, see, Scopes, 1987, Protein Purification: Principles and Procedure, 2nd Ed., C.R. Cantor ed., Springer Verlag, New York, New York, and Parvez et al., 1985, Progress in HPLC, Vol. 1, Science Press, Utrecht, The Netherlands).

[0140] Recombinant expression techniques can be applied to obtain the Cell proteins, derivatives, and analogues of the invention (see, e.g., Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory, 2d Ed., Cold Spring Harbor, New York; Glover, D.M. ed., 1985, DNA Cloning: A Practical Approach, MRL Press, Ltd., Oxford, U.K., Vol. I, II). The nucleotide sequence of *cel1* is set forth in SEQ ID NO:2. An *cel1* clone can be isolated using well-known techniques in the art, such as by screening a library, chemical synthesis, or polymerase chain reaction (PCR). Cloned *cel1* gene sequences can be modified by any of numerous strategies known in the art.

[0141] To produce a recombinant Cel1 protein, derivative or analogue, a nucleic acid sequence encoding the Cel1 protein, derivative or analogue is operatively linked to a promoter such that the Cell protein, derivative, or analogue is produced from said sequence. For example, a vector can be introduced into a cell, within which cell the vector or a portion thereof is expressed, producing Cel1 or a portion thereof. In a preferred embodiment, the nucleic acid is DNA if the source of RNA polymerase is DNA-directed RNA polymerase, but the nucleic acid may also be RNA if the source of polymerase is RNA-directed RNA polymerase or if reverse transcriptase is present in the cell or provided to produce DNA from the RNA. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art.

[0142] A method for the production of Cell comprises: (a) culturing a host cell containing a recombinant expression vector, said vector comprising a nucleotide se-

quence encoding Cel1 under conditions such that Cel1 is expressed by the cell; and (b) recovering Cell expressed by the cell.

[0143] A variety of host-vector systems may be utilized to express the protein-coding sequence. These include, but are not limited to, mammalian cell systems infected with virus (e.g., vaccinia virus, adenovirus, etc.); insect cell systems infected with virus (e.g., baculovirus); microorganisms such as yeast containing yeast vectors, or bacteria transformed with bacteriophage, DNA, plasmid DNA, or cosmid DNA. The expression elements of vectors vary in their strengths and specificities and depending on the host-vector system utilized, any one of a number of suitable transcription and translation elements may be used.

[0144] Expression of a Cell protein, derivative, or analogue may be controlled by any promoter/enhancer element known in the art. Such promoters include, but are not limited to: the SV40 early promoter region (Bernoist and Chambon, 1981, Nature 290:304-310), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto et al., 1980, Cell 22:787-797), the HSV-1 (herpes simplex Virus-1) thymidine kinase promoter (Wagner et al., 1981, Proc. Natl. Acad. Sci. USA 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster et al., 1982, Nature 296:39-42); prokaryotic expression vectors such as the β-lactamase promoter (Villa-Kamaroff et al., 1978, Proc. Natl. Acad. Sci. USA 75:3727-3731), or the tac promoter (DeBoer et al., 1983, Proc. Natl. Acad. Sci. USA 80:21-25); see also "Useful proteins from recombinant bacteria" in Scientific American, 1980, 242:74-94; plant expression vectors comprising the *cel1* promoter or functional fragments thereof, the nopaline synthetase promoter region (Herrera-Estrella et al., Nature 303:209-213) or the cauliflower mosaic virus 35S RNA promoter (Gardner et al., 1981, Nucl. Acids Res. 9:2871), and the promoter of the photosynthetic enzyme ribulose biphosphate carboxylase (Herrera-Estrella et al., 1984, Nature 310:115-120); promoter elements from yeast or other fungi such as the Gal 4 promoter, the ADC (alcohol dehydrogenase) promoter, PGK (phosphoglycerol kinase) promoter, alkaline phosphatase promoter, and the following animal transcriptional control regions, which exhibit tissue specificity and have been utilized in transgenic animals: elastase I gene control region which is active in pancreatic acinar cells (Swift et al., 1984, cell 38:639-646; ornitz et al., 1986, Cold Spring Harbor Symp. Quant. Biol. 50:399-409; MacDonald, 1987, Hepatology 7:425-515); insulin gene control region which is active in pancreatic beta cells (Hanan, 1985, Nature 315:115-122), immunoglobulin gene control region which is active in lymphoid cells (Grosschedl et al., 1984, Cell 38:647-658; Adames et al., 1985, Nature 318:533-538; Alexander et al., 1987, Mol. Cell. Biol. 7:1436-3444), mouse mammary tumor virus control region which is active in testicular, breast, lymphoid and mast cells (Leder et al., 1986, Cell 45:485-495), albumin gene control region which is active in liver (Pinkert et al.,

1987, Genes and Devel. 1:268-276), alpha-fetoprotein gene control region which is active in liver (Krumlauf et al., 1985, Mol. Cell. Biol. 5:1639-1648; Hammer et al., 1987, Science 235:53-58; alpha 1-antitrypsin gene control region which is active in the liver (Kelsey et al., 1987, Genes and Devel. 1:161-171), beta-globin gene control region which is active in myeloid cells (Mogam et al., 1985, Nature 315:338-340; Kollias et al., 1986, Cell 46:89-94; myelin basic protein gene control region which is active in oligodendrocyte cells in the brain (Readhead et al., 1987, Cell 48:703-712); myosin light chain-2 gene control region which is active in skeletal muscle (Sani, 1985, Nature 314:283-286), and gonadotropic releasing hormone gene control region which is active in the hypothalamus (Mason et al., 1986, Science 234:1372-1378). The promoter element which is operatively linked to the nucleic acid encoding a Cel1 protein, derivative or analogue can also be a bacteriophage promoter with the source of the bacteriophage RNA polymerase expressed from a gene for the RNA polymerase on a separate plasmid, e.g., under the control of an inducible promoter, for example, the nucleic acid encoding chemokine, derivative, or analogue, operatively linked to the T7 RNA polymerase promoter with a separate plasmid encoding the T7 RNA polymerase.

[0145] In addition, a host cell strain may be chosen which modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Expression from certain promoters can be elevated in the presence of certain inducers; thus, expression of the genetically engineered chemokine, derivative or analogue may be controlled. Furthermore, different host cells have characteristic and specific mechanisms for the translational and post-translational processing and modification (e.g., glycosylation, phosphorylation of proteins). Appropriate cell lines or host systems can be chosen to ensure the desired modification and processing of the foreign protein expressed. For example, expression in a bacterial system can be used to produce an unglycosylated core protein product. Expression in yeast or insect cells will produce a glycosylated product. Expression in mammalian or plant cells can be used to ensure "native" glycosylation of a heterologous protein. Furthermore, different vector/host expression systems may effect processing reactions to different extents.

[0146] The Cel1-encoding nucleic acid sequence can be mutated *in vitro* or *in vivo*, to create and/or destroy translation, initiation, and/or termination sequences, or to create variations in coding regions. Any technique for mutagenesis known in the art can be used, including, but not limited to, *in vitro* site-directed mutagenesis (Hutchinson et al., 1978, J. Biol. Chem. 253:6551), use of TAB® linkers (pharmacia), mutation-containing PCR primers, etc.

[0147] The experimentation involved in mutagenesis consists primarily of site-directed mutagenesis followed by phenotypic testing of the altered gene product. Some

of the more commonly employed site-directed mutagenesis protocols take advantage of vectors that can provide single stranded as well as double stranded DNA, as needed. Generally, the mutagenesis protocol with such vectors is as follows. A mutagenic primer, *i.e.*, a primer complementary to the sequence to be changed, but consisting of one or a small number of altered, added, or deleted bases, is synthesized. The primer is extended *in vitro* by a DNA polymerase and, after some additional manipulations, the now double-stranded DNA is transfected into bacterial cells. Next, by a variety of methods, the desired mutated DNA is identified, and the desired protein is purified from clones containing the mutated sequence. For longer sequences, additional cloning steps are often required because long inserts (longer than 2 kilobases) are unstable in those vectors. Protocols are known to one skilled in the art and kits for site-directed mutagenesis are widely available from biotechnology supply companies, for example from Amersham Life Science, Inc. (Arlington Heights, IL) and Stratagene Cloning Systems (La Jolla, CA).

[0148] The Cel1 derivative or analogue may be expressed as a fusion, or chimeric protein product (comprising the protein, fragment, analogue, or derivative joined via a peptide bond to a heterologous protein sequence (of a different protein)). Such a chimeric product can be made by ligating the appropriate nucleic acid sequences encoding the desired amino acid sequences to each other by methods known in the art, in the proper coding frame, and expressing the chimeric product by methods commonly known in the art.

[0149] In addition, Cel1 proteins, derivatives (including fragments and chimeric proteins), and analogues can be chemically synthesized. See, e.g., Clark-Lewis et al., 1991, Biochem. 30:3128-3135 and Merrifield, 1963, J. Amer. Chem. Soc. 85:2149-2156. For example, Cel1, derivatives and analogues can be synthesized by solid phase techniques, cleaved from the resin, and purified by preparative high performance liquid chromatography (e.g., see Creighton, 1983, Proteins, Structures and Molecular Principles, W.H. Freeman and Co., N.Y., pp. 50-60). Cel1, derivatives and analogues that are proteins can also be synthesized by use of a peptide synthesized. The composition of the synthetic peptides may be confirmed by amino acid analysis or sequencing (e.g., the Edman degradation procedure; see Creighton, 1983, Proteins, Structures and Molecular Principles, W.H. Freeman and Co., N.Y., pp. 34-49).

[0150] The Cel1 proteins, derivatives; or analogues of the invention may be synthesized in their entirety by the sequential addition of amino acid residues or alternatively as fragment subcomponents which may be combined using techniques well known in the art, such as, for example, fragment condensation (Shin et al., 1992, Biosci. Biotech. Biochem. 56:404-408; Nyfeler et al., 1992, Peptides, Proc. 12th Amer. Pep. Soc., Smith and Rivier eds., Leiden, pp. 661-663); and Nokihara et al., 1990, Protein Research Foundation, Yanaihara ed., Osaka,

pp 315-320).

[0151] Cel1 derivatives can be obtained by proteolysis of the protein followed by purification using standard methods such as those described above (e.g., immunoaffinity purification).

5.4. APPLICATIONS

[0152] The present invention finds use in various applications, including but not limited to, those listed hereinbelow.

[0153] First, the present invention can be used to provide fast growing transgenic forest trees for the evergrowing pulp and paper industry, thereby reducing the devastating ecological effects associated with rain forest exhaustion.

[0154] Second, the present invention can be used to provide transgenic plants with modified cell walls possessing different properties, such as, but not limited to, plants having longer or shorter fibers; plants which are either more or less resistant to biodegradation; plants which are either more or less digestible in the rumen of animals; and plants which are either more or less resistant to pests, such as insects, fungi, viruses and bacteria.

[0155] Third, the present invention can be used to provide transgenic plants with useful fibers such as; cotton, flax, etc. that produce higher yields of modified fibers which have longer or shorter fibers; or have modified properties such as "look", absorbency, strength and reology of the chemically modified cellulose.

[0156] Fourth, the present invention can be used to provide transgenic plants having increased starch production and/or content.

[0157] Fifth, the present invention can be used to provide transgenic plants having increased heat resistance.

[0158] The present invention can be further used to provide transgenic fruiting plants, such as tomato plants, etc., the fruits thereof having higher cellulose content, as well as higher sugar content, which can be used in the ketchup and tomato puree industry. The present invention can also be used to provide transgenic potato plants with faster growing canopies and shorter life cycles which result in shorter time between planting and harvesting, and/or higher tuber yield. The present invention can further be used to provide transgenic flowering plants having longer or shorter stems, larger or smaller petals, etc. In addition, the invention can be used to provide fast growing rice that will emerge more quickly from the water and thus, have an increased survival rate and yield. Furthermore, the present invention can be used to provide lettuce plants featuring larger or smaller leaves. And finally, the invention can be used to provide forage crops, such as alfalfa, clover, etc., with higher biomass and/or modified digestibility in rumen animals.

[0159] A further utility of the present invention is to improve the rate of growth of naturally occurring metal or toxin hyperaccumulating plants to increase their biomass thereby improving the rate or extent of phytoremediation.

(See Glass, October 1, 1997, Genetic Engineering News, p. 8, 41-43).

[0160] The cell gene described herein has utility as a transgene encoding cell wall modulation protein or polypeptide in a transgenic plant to alter plant structure or morphology. The cell gene also has utility for encoding the Cel1 protein in recombinant vectors which may be inserted into host cells to express the cell protein. Further, the cell gene may be utilized (1) as a nucleic acid probe to screen nucleic acid libraries to identify other endo-1,4- β -glucanase genes or mutants; (2) as a nucleic acid sequence to be mutated or modified to produce Cell protein variants or derivatives; (3) isolation of the nucleic acid sequence encoding the Cel1 secretion signal peptide; and (4) as a nucleic acid encoding endo-1,4- β -glucanase in molecular biology techniques or industrial applications commonly known to those skilled in the art.

[0161] The cell nucleic acid molecules may be used as plant cell antisense molecules, useful, for example, in plant *cel1* gene regulation or as antisense primers in amplification reactions of plant *cel1* gene nucleic acid sequences. With respect to plant *cel1* gene regulation, such techniques can be used to regulate, for example, plant growth, development or gene expression. Further, such sequences may be used as part of ribozyme and/or triple helix sequences, also useful for *cel1* gene regulation.

[0162] The *cel1* promoter described herein may be utilized as an elongating tissue specific plant promoter to express any protein, polypeptide or peptide of interest in a tissue specific manner in a transgenic plant. In particular, the *cel1* promoter may be used to express a cell wall modulation protein or polypeptide in an elongating tissue specific manner to produce transgenic plants having altered structure. Further, the *cel1* promoter can be used to express any CBD in elongating tissues of transgenic plants to produce plants having altered structure.

[0163] The *Arabidopsis thaliana* Cel1 protein of the invention can be used in any biochemical applications (experimental or industrial) where endo-1,4- β -glucanase activity is desired, for example, but not limited to, digestion of polysaccharides, modification of cellulose, modification of elongating plant structures, and experimental or industrial biochemical applications known to those skilled in the art.

[0164] The Cell secretion signal peptide described herein may be utilized to facilitate the cellular secretion of any protein, polypeptide or peptide of interest by constructing recombinant nucleic acids encoding the Cell secretion signal peptide fused to a sequence encoding a protein of interest, and expressing the recombinant proteins.

[0165] The following examples are presented for purposes of illustration only and are not intended to limit the scope of the invention in any way.

6. EXPERIMENTAL PROTOCOLS OF THE EXAMPLES

[0166] The following protocols and experimental ma-

terials were employed in the Examples that follow.

6.1. PLANT MATERIAL AND GROWTH CONDITIONS

[0167] *Arabidopsis thaliana* cv. Columbia and *Nicotiana tabaccum*-SR1 (tobacco) plants were grown at 24-25°C under a 16 h photoperiod, using cool-white fluorescent light (50-60 $\mu\text{E m}^{-2} \text{S}^{-1}$). Dwarf *A. thaliana* plants were produced by treating the potting mixture prior to seeding with 250 ppb uniconazole [(E)-1-(4-chlorophenyl)-4,4-dimethyl-2-(1,2,4-triazol-1-yl)penten-3-ol] (Agan chemicals Inc., Israel), a gibberellin biosynthesis inhibitor (Henry, 1985, Bull. Plant Growth Regul. Soc. Am. 13:9-11).

6.2. ISOLATION OF PLANT NUCLEIC ACIDS FROM PLANT TISSUE

[0168] DNA was extracted from stems and leaves of *Arabidopsis thaliana* cv. Columbia as described by Doyle and Doyle (1987, Phytochem. Bull. 19:11-15). RNA was extracted from elongating stems with "TRI-REAGENT™" (Molecular Research Center Inc., Cincinnati, OH), according to the manufacturer's instructions.

6.3. PCR AMPLIFICATION OF THE EGASE DNA PROBE FROM CHROMOSOMAL DNA

[0169] Degenerate primers (Compton, 1990, "Degenerate primers for DNA amplification," in PCR Protocols: A Guide to Methods and Applications, Innis, Gelfand, Sninsky, and White eds., Academic Press, San Diego, CA) were synthesized based on two conserved amino acid regions, GGYDA (SEQ ID NO:10) and CW-ERPDM (SEQ ID NO:11), from avocado and tomato cellulase amino acid sequences (Tucker and Milligan, 1991; Lashbrook et al., 1994).

[0170] Primer #1 GGYDA (SEQ ID NO:10): 5'-GAATTCGGA(T/C/G)GGA(T/C/G)TAT(C)TAT(C)GAC(T)GC-3' (SEQ ID NO:12). Primer #2 CWERPDM (SEQ ID NO:12): 5'-GAATTCATA(G)TCT(C)TCA(G/C/T)GGA(T/C/G)CGT(C)TCCAA(G)CA-3' (SEQ ID NO:13).

[0171] The PCR mix contained 2 μl chromosomal DNA (0.5 $\mu\text{g}/\mu\text{l}$), 2.5 ml 10X Tag Polymerase buffer (Promega, Madison, Wisconsin), 1 μl dNTP mix (10 mM), 1.5 μl 25 mM MgCl_2 , 0.5 μl (25 μM) of each primer, 1 unit *Taq* polymerase (Promega, Madison, Wisconsin) and double distilled H_2O (dd H_2O) to a final volume of 25 μl . Mineral oil (25 μl) was added to prevent evaporation. The PCR program was as described in Compton (1990, "Degenerate primers for DNA amplification" in PCR Protocols: A Guide to Methods and Applications, pp 39-45, eds Innis, Gelfand, Sninsky, and White, Academic Press, San Diego, California).

[0172] A fragment of 260 bp amplified by the PCR reaction was purified on a 2% (w/v) agarose/TBE gel as described in Sambrook et al., (1989, Molecular Cloning:

A Laboratory Manual, Cold Spring Harbor Laboratory Press, New York) and is shown in FIG. 1. The isolated 260 bp fragment was digested with *Eco*RI and cloned into the *Eco*RI cloning site of the M13 RF DNA mpl8 vector (New England Biolabs, Beverly, Massachusetts).

6.4. CLONING OF A. THALIANA GENOMIC EGASE GENE

[0173] The genomic clone of EGase was isolated using an *A. thaliana* genomic library packaged in the vector EMBL3 (Promega, Madison, Wisconsin). The library was constructed from *A. thaliana* genomic DNA partially digested with *Sau*A3 and cloned into the *Bam*HI cloning site of the EMBL3 vector. A total of 2.5×10^5 plaques were screened using the PCR-derived DNA EGase probe (260 bp PCR fragment, FIG. 1) according to Sambrook et al. (1989). A single hybridizing recombinant phage was detected and purified to homogeneity. Fragments containing the EGase gene within the X genomic clones or subsequent plasmid subclones of pUC18 (New England Biolabs, Beverly, Massachusetts) were localized by Southern blot analysis (Southern, 1975, J. Mol. Biol. 98:503-517). Overlapping serial deletions of genomic subclones were generated by *Exo*III digestion of the subclones as shown in the gene construction scheme set forth in FIG. 2. The *Arabidopsis* EGase sequence (*cel1*) was deposited under the non-disclosure terms in the EMBL Nucleotide Sequence Submissions, European Bioinformatics Institute, Hinxton Hall, Hinxton, Cambridge, and was given the accession #X98543 (SEQ ID NO:9).

6.5. CLONING *cel1* cDNA

[0174] RNA extracted from elongating stems of *A. thaliana* was used as a template for the reverse transcriptase polymerase chain reaction (RT-PCR kit, Stratagene, La Jolla, California). Total cDNA was used for the PCR reaction. Two specific primers were designed according to the terminal exon sequences. Primer #3: 5'-ATGGCGCGAAAATCCCTAAT-3' (SEQ ID NO:14) also (nucleotides 1666 - 1685 in SEQ ID NO:9); and Primer #4: 5'-TCATCGCCAAGTAGAA-3' (SEQ ID NO:15) also (nucleotides 5258-5273 in SEQ ID NO:9). The resulting 1.5 kb PCR fragment (FIG. 3) was cloned into the pGEM-T Vector system (Promega, Madison, Wisconsin) and sequenced. This sequence was deposited under the non-disclosure terms in the EMBL Nucleotide Sequence Submissions, European Bioinformatics Institute, Hinxton Hall, Hinxton, Cambridge, and was given the accession #X98544 (SEQ ID NO:2).

6.6. NUCLEOTIDE SEQUENCE DETERMINATIONS

[0175] Nucleotide sequences were determined using an automated sequencer Model 373 (Perkin-Elmer, California, USA), according to the manufacturer's instruc-

tions.

6.7. NORTHERN BLOT ANALYSIS

[0176] A 768 bp DNA probe, (starting at nucleotide 399 of SEQ ID NO:2) generated from the cell cDNA clone (SEQ ID NO:2) was used for northern blot analysis. In each experiment, 40-50 *A. thaliana* plants were used to extract total RNA from the following tissues: fully expanded leaves, basal internode of flowering stems, the elongation zone in the flowering stem of normal plants and the elongation zone in the flowering stem of dwarf plants (treated with uniconazole as described above).

[0177] Total RNA (10 µg) was separated on a 1.6% agarose gel and transferred to a "HYBOND-N⁺" membrane (Amersham, United Kingdom). The DNA probe was ³²P-labeled by the "REDI PRIMETM" kit (Random Prime Labeling Kit, Amersham, United Kingdom). The membranes were hybridized at 55°C for 16 hr. The final wash was carried out in 0.5 X SSC, 0.1% (w/v) SDS for 10 min at 60°C. The 18S rRNA probe was used as an internal standard. RNA levels were determined using densitometry.

6.8. CONSTRUCTION OF *cel1* PROMOTER-gus BINARY VECTOR (pPCGUS)

[0178] A DNA fragment which includes the *cel1* promoter region of *A. thaliana* endo-1,4-β-glucanase (*cel1*, nucleotides 5-1618 of SEQ ID NOs:1 or 9) was cloned into pUC18 (New England Biolabs, Beverly, Massachusetts). Briefly, a PCR fragments was generated using the following primers: #5 (*HindIII*): 5'-AAAAAAGCTTACCTGCAGGTCAACGG-3' (SEQ ID NO:16), and #10 (*Sall*): 5'-AAAAGTCGACGAAGGTGATAGGACCAAC-3' (SEQ ID NO:6), digested with restriction endonucleases *HindIII* and *Sall*, and cloned into the *HindIII* and *Sall* cloning sites of pUC18 (New England Biolabs Beverly, Massachusetts). A 1.6 kb *HindIII*-*Sall* fragment excised from the above construct was subcloned into the *HindIII* and *Sall* cloning sites of the binary vector pBI101 (Clontech, Palo Alto, California), at the 5' end of the *gus* gene (Jefferson, 1987, Plant Mol. Biol. Rep. 5:387-405) and designated pPCGUS.

6.9. CONSTRUCTION/TRANSGENIC PLANTS EXPRESSING *cel1* PROMOTER-gus FUSION

[0179] The above construct, i.e. pPCGUS was mobilized into disarmed LB 4404 *Agrobacterium tumefaciens* by triparental mating (An, 1987, Meth. Enzymol. 153: 292-305). Leaf-disc transformation was performed with *Nicotiana tabacum*-SR1 plants as described previously (DeBlock et al., 1984, EMBO J. 3:1681). Regenerated transgenic plants were selected on kanamycin. F₁ seeds from eight independent plants transformed with the construct were used for the functional assays.

[0180] The plants were analyzed for the presence of

the putative *cel1* promoter region by southern blot. As a control for basal levels of GUS activity in tobacco, plants were transformed with the promoterless pBI101. Transgenic plants were grown in the greenhouse at 25°C under a 16 hr photoperiod.

6.10. HISTOLOGICAL GUS STAINING ANALYSIS OF TRANSGENIC PLANTS

[0181] GUS staining was performed with X-Gluc as described previously (Jefferson et al., 1987, Plant Mol. Biol. Rep. 5:387-405). Ten day old seedlings were incubated overnight with X-Gluc at 37°C and then kept in a 70% ethanol solution. Prior to being photographed, the plants were incubated for few minutes in 90% lactic acid at 90°C and then cooled to room temperature for 2 hr.

6.11. CONSTRUCTION OF *cel1* PROMOTER-*cel1* SIGNAL-*cbd* BINARY VECTOR (pCC1)

[0182] A DNA fragment which includes the *cel1* promoter region and encodes the *cel1* signal peptide, i.e., part of *A. thaliana* endo-1,4-β-glucanase (*cel1*, nucleotides 5-1770 of SEQ ID NOs: 1 or 9) was cloned into pUC18 (New England Biolabs, Beverly, Massachusetts). Briefly, a PCR fragment was generated, using the following primers: #5 (*HindIII*) 5'-AAAAAAGCTTACCTGCAGGTCAACGG-3' (SEQ ID NO: 16), and #6 (*Sall*): 5'-AAACTCGACTTTACGAGAGCGTCGC-3' (SEQ ID NO: 17) digested with restriction endonucleases *HindIII* and *Sall*, and was cloned into the *HindIII* and *Sall* cloning sites of pUC18 (New England Biolabs, Beverly, Massachusetts).

[0183] A cellulose binding domain DNA fragment containing the nucleotide sequence encoding a fragment of the *cbpA* protein of *clostridium cellulovorans* (said cellulose binding domain herein referred to as "cbd") (see Pat. No. 5,496,934) (nucleotides 3-494 of SEQ ID NO:5) was generated by PCR amplification using the following primers: #7 (*Sall*) 5'-AAAAGTCGACATGGCAGCGACATCATCAA-3' (SEQ ID NO:18) and #8 (*BamHI*) 5'-AAAAGGATCCCTATGGTGTGTACCAAG-3' (SEQ ID NO:19), which included *Sall* and *BamHI* restriction sites.

[0184] Following digestion with *Sall* and *BamHI* restriction endonucleases, the *cbd* coding DNA fragment was cloned into the *Sall* and *BamHI* sites of the above modified pUC18 vector, fused to, and in frame with, the signal peptide of cell.

[0185] The primer for the C-terminal end of the *cbd* gene contained a stop codon. The *Sall* site between the two fragments adds two in frame amino acids: Valine and Asparagine, which are present between the *cel1* signal peptide and the *cbd* coding regions.

[0186] A *HindIII*-*SacI* DNA fragment containing the cell promoter region, the *cel1* signal peptide and the fused *cbd*, in that order, was subcloned into the binary vector pBI101 (Clontech, Palo Alto, California) which was predigested with *HindIII* and *SacI*. This vector was designat-

ed pCC1.

6.12. CONSTRUCTION OF CaMV35S Ω PROMOTER-*cel1* SIGNAL-cbd BINARY VECTOR (p35SC1)

[0187] A vector containing the CaMV35S Ω promoter fused to the *cel1* signal sequence and to the *cbd* sequence was constructed as follows. A DNA fragment encoding the *cel1* signal peptide (nucleotides 1-105 of SEQ ID NO:2) was cloned into pUC18 (New England Biolabs, Beverly, Massachusetts). Briefly, a PCR fragment of *cel1* was generated using the following primers: #9 (*SphI*) 5'-AAAAGCATGCCGCGAAAATCCCTAATTT-3' (SEQ ID NO:20) and #6 (*Sall*) : 5'-AAAAGTCGACTTTACGGA-GAGCGTCGC-3' (SEQ ID NO:17); digested with restriction endonucleases *SphI* and *Sall*, and cloned into the *SphI* and *Sall* cloning sites of pUC18. Inclusion of the *SphI* restriction site replaced the first amino acid after the initiation site from Alanine to Proline. In addition, the primer for the C-terminal end of the *cbd* gene contained a stop codon. The *Sall* site between the two fragments adds two in frame amino acids: Valine and Asparagine, which are present between the *cel1* signal peptide and the *cbd* coding regions.

[0188] A *cbd* encoding DNA fragment (nucleotides 3-494 SEQ ID NO:5) was generated by PCR amplification using the following primers: #7 (*Sall*) 5'-AAAAGTC-GACATGGCAGCGACATCATCAA-3' (SEQ ID NO:18) and #10 (*EcoRI*) 5'-AAAAGAATTCCTATGGTGC TG-TACCAAG-3' (SEQ ID NO:21), which included *Sall* and *EcoRI* restriction sites.

[0189] Following *Sall* and *EcoRI* restriction, the *cbd* encoding DNA fragment was cloned into the *Sall* and *EcoRI* sites of the above modified pUC18 vector, fused to, and in frame with, the signal peptide of *cel1*.

[0190] The DNA containing the *cel1* signal-*cbd* fusion was cloned into pCd cloning cassette (Broido et al., 1993, *Physiologia Plantarum* 88:259-266) using the *SphI* and *EcoRI* cloning sites. The pCd cassette contains a polylinker down stream of a CaMV35S promoter (Guilley et al., 1982, *Cell* 30:763-773) and the Ω DNA sequence from the coat protein gene of tobacco mosaic virus (Gallie et al., 1987, *Nucl. Acid Res.* 15:3257-3273). A DNA fragment containing a CaMV35S Ω *cel1*-signal peptide-*cbd* and the octopine polyadenylation site was excised using *BamHI* and *SacI* and was subcloned into the *BamHI* and *SacI* cloning sites of the binary vector pBI101 (Clontech, Palo Alto, California). The resulting vector was designated p35SC1.

6.13. CONSTRUCTION OF *cbd* TRANSGENIC PLANTS

[0191] The binary vectors (p35SC1, pCC1 and pBI101, as a control) were mobilized into disarmed LB 4404 *Agrobacterium tumefaciens* by triparental mating (An, 1987, *Meth. Enzymol.* 153: 292-305). Leaf-disc transformation was performed with *Nicotiana tabacum*-SR1 plants as described previously (DeBlock et al., 1984, *EMBO J.*

3:1681). Regenerated transgenic plants were selected on kanamycin. F₁ Seeds were collected from independent plants transformed with each one of the vectors. The plants were analyzed by Southern blot (Sambrook et al., 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, New York; Southern, 1975, *J. Mol. Biol.* 98:503-517) and PCR using primers #7 and #8 (SEQ ID NOs:18 and 19, respectively). Transgenic plants were grown in the greenhouse at 25°C under a 16 hr photoperiod.

6.14. TRANSCRIPTION ANALYSIS OF *cbd*

[0192] To determine transcription of the *cbd* transgene, RNA extracted from elongating stems and young leaves was used as a template for reverse transcriptase reaction (RT-PCR kit) (Stratagene, La Jolla, California). The total cDNA was used for the PCR amplification using primers #7 and #8 (SEQ ID NOs:18 and 19, respectively).

7. EXAMPLE: CLONING OF *ARABIDOPSIS THALIANA* EGASE DNA PROBE

[0193] The EGase gene, *i.e.*, *cel1* of *A. thaliana* was isolated. Considerable homology exists between the different EGase genes from different plants (Lashbrook et al., 1994, *Plant Cell* 6:1485-1493; Tucker and Milligan, 1991 *Plant Physiol.* 95:928-933; Wu et al., 1996, *Plant Physiol.* 110:163-170). Degenerate primers (SEQ ID NOs: 12 and 13) were synthesized based on two conserved regions from avocado and tomato cellulase amino-acid sequences (Lashbrook et al., 1994, *Plant Cell* 6:1485-1493; Tucker and Milligan, 1991, *Plant Physiol.* 95:928-933) and enabled the amplification of a 260 bp PCR fragment which served as a probe to clone a genomic *cel1* from *A. thaliana*. These primers have been used successfully in the past in the isolation of several DNA fragments from mung bean that encode EGase genes (Shoseyov, L., 1992, "Endo-1,4- β -glucanase gene expression during adventitious root formation in Mung bean cuttings," Master thesis, the Hebrew University of Jerusalem).

[0194] PCR amplification was performed using chromosomal DNA as the template and two degenerate primers designed according to conserved amino-acid sequences in avocado and tomato EGases (Lashbrook et al., 1994, *The Plant Cell* 6:1485-1493; Tucker and Milligan, 1991, *Plant Physiol.* 95:928-933). PCR amplification resulted in two DNA fragments of about 260 and 370 bp (FIG. 1). The isolated 260 bp fragment was cloned into M13 mp18. single stranded DNA was then used for sequence analysis. The deduced amino-acid sequence of the 260 bp fragment revealed 62% homology to the avocado EGase.

8. EXAMPLE: ISOLATION AND CHARACTERIZATION OF THE EGASE GENOMIC CLONE

[0195] A comparison of the *A. thaliana cel1* genomic gene with avocado *cel1* reveals that exons 2 and 3 of the avocado gene are intercepted by a large intron. This intron does not exist in *A. thaliana cel1*. The *A. thaliana cel1* DNA gene encoded a 54-kDa protein. A sequence comparison with avocado EGase revealed 56% sequence identity (FIG. 4). Furthermore, a high degree of conservation was found in the number and positions of the cysteine residues between the proteins, suggesting a conserved tertiary structure. This was also supported by comparing Kyte-Doolittle hydropathy analyses of *A. thaliana* Cell and avocado EGase (Cell) (FIG. 5). The cell deduced amino-acid sequence contained one potential glycosylation site. A 17 amino acid motif which classifies Cell in the E family of glycosidases was also detected (see generally, Gilkes et al., 1991, Microbiol. Rev. 55:303-315 regarding glycosidases). The first 25 amino acids at the N-terminus were hydrophobic, including a positively charged arginine residue near the very end of the N-terminus, as expected in a typical signal-peptide sequence (non Heijne et al., 1983, Eur. J. Biochem. 133:17-21).

[0196] An *A. thaliana* genomic library was screened to isolate the genomic *cel1* gene. One positive clone was isolated from a total of 2.5×10^5 recombinant plaque-forming units screened using the 260 bp PCR fragment (FIG. 1) as a probe. *SalI* digestion of the positive clone, followed by Southern blot analysis, revealed a 7.5-kb fragment. A restriction map of the *SalI* DNA fragment is presented in FIG. 2. Three different subclones were constructed in pUC18 as further depicted in FIG. 2. *ExoIII* deletions followed by sequence analysis revealed the primary DNA sequence of the full-length *cel1* gene. As represented in FIG. 2, the gene consists of seven exons intercepted by six introns.

9. EXAMPLE: ISOLATION AND CHARACTERIZATION OF *cel1* cDNA

[0197] RT-PCR was used to test for the presence of *cel1* mRNA in elongating tissue and to isolate the full-length cDNA. The *cel1* 1.5-kb cDNA fragment (FIG. 3) was successfully cloned and sequenced (SEQ ID NO:2). The cDNA sequence perfectly matched the DNA sequence of the combined exons (nucleotides 1666-1875, 1959-2366, 2747-2386, 2936-3097, 4383-4493, 4661-4825 and 4941-5270 of SEQ ID NO:9). Several sequence discrepancies were found between the 260-bp DNA probe and cell cDNA. At this point it was not determined if these changes represent different genes or simply PCR derived mutations. The 1476 bp open reading frame (nucleotides 1-1476, SEQ ID NOs:2 and 3) was found to encode a 492 amino acid polypeptide (SEQ ID NO. 4) with a predicted molecular weight of 54 kDa. Sequence comparison with avocado EGase revealed 56%

identity (FIG. 4). A comparison of Kyte-Doolittle hydropathy analyses (Kyte and Doolittle, 1982, J. Mol. Biol. 157:105-132) of *A. thaliana* Cell and avocado EGase (Cell) is presented in FIG. 5.

10. EXAMPLE: RNA TRANSCRIPT LEVELS OF *cel1* IN DIFFERENT TISSUES OF *ARABIDOPSIS*

[0198] Northern blot analysis of *cel1* was carried out using the 768-bp *cel1* cDNA fragment as a probe (FIG. 6). RNA transcripts were undetectable in fully expanded leaves, as well as at the basal internode of flowering stems of normal *A. thaliana* plants. However a strong transcript signal was detected in the elongating zone of flowering stems of normal plants. *A. thaliana* plants that were treated with uniconazole produced dwarf plants. The level of *cel1* RNA transcript in the elongating zone of dwarf flowering stems was significantly lower than that in the normal plants (FIG. 6). Densitometry analysis of northern blots from three independent experiments revealed a 2-5 fold difference between the transcript levels of nominal versus dwarf plants.

11. EXAMPLE: HISTOLOGICAL GUS STAINING ANALYSIS OF TRANSGENIC PLANTS

[0199] Transgenic tobacco plants transformed with the putative cell promoter region (nucleotides 5-1618, SEQ ID NO:1) fused to the *gus* reporter gene in the pBI101 binary expression vector (Clontech, Palo Alto, California), were tested for tissue-specific expression. Significant GUS activity was observed in sixteen seedlings that were generated from eight independent transgenic plants. Staining was observed both in shoot and root elongating zones (FIGS. 7A-C). Young leaves, although to a less extent, were also stained (not shown). Control transgenic plants containing the same construct without the putative cell promoter region, did not show any GUS staining.

12. EXAMPLE: CONSTRUCTION OF *cbd* TRANSGENIC TOBACCO PLANTS

[0200] Fifteen to twenty independent transgenic tobacco plants (F_0 , parental generation) were prepared from each one of the vectors pCCI, p35SC1 and pBI101. pBI101 served as a negative control as it does not encode for *cbd*. Confirmation of the presence of a transgene was conducted by PCR analysis (see, for example, FIG. 9), Southern blot analysis (not shown), and kanamycin resistance. The results indicated the presence of a single copy of the *cbd* construct in the F_0 generation for both the pCCI and p35SC1 constructs, and of at least two copies for the pBI101 in the control plants. Transcription of *cbd* in both pCCI and p35SC1 transgenic plants was confirmed by RT-PCR analysis (see, for example, FIG. 10).

[0201] F_1 transgenic tobacco plants transformed with

either pCCI or p35SC1 (the latter are shown in FIG. 11B) displayed great size variation. As shown in FIG. 11A, the F₁ control plants transfected with pBI101 showed very moderate variation. In the latter case no kanamycin sensitive plants were observed, indicating the presence of more than a single active copy of the transgene, each of the copies independently segregates.

[0202] F₁ transgenic tobacco plants of a parent transformed with a single copy of either pCCI or p35SC1 segregated into three distinct phenotypes. About a quarter of the F₁ plants were kanamycin sensitive, indicating absence of the transgene. An additional quarter of the plants had a small phenotype, whereas about half of the plants had a large phenotype. The two later segregates further exhibited phenotypic variation. Among the small plants, some exhibited distorted hypocotyls at the early stages of germination. Among the large plants, variation was from normal size (as compared to kanamycin grown pBI101 control transgenic plants) to giant size. Collectively, these results indicate that the kanamycin sensitive plants were homozygous for the absence of the transgene, the large plants were heterozygotes, whereas the small plants contained two active copies of the transgene. These results are in very good correlation with the report (PCT Publication WO 94/24158) demonstrating that high concentrations of cbd protein inhibit plant growth *in vitro*, whereas, moderate concentrations accelerate plant growth. When grown without kanamycin, F₁ transgenic tobacco plants transformed with either pCCI or p35SC1 segregated into the large and small phenotypes. Under these growth conditions, the kanamycin sensitive plants could not be distinguished from the subpopulation of heterozygous normal size plants of the large phenotype. These results confirm that *cbd* genotype is responsible for the observed phenotypes, *i.e.*, expression of *cbd* in transgenic plants modulates their growth.

[0203] The difference in size among the phenotypically distinct groups (large and small) was also maintained after maturation (FIG. 12).

[0204] Furthermore, transgenic plants that were vegetatively propagated maintained their phenotype while young (FIG. 13) as well as in a later stage of their vegetative development (FIG. 14). These results demonstrate that *cbd* transgenic plants exhibiting an altered growth phenotype, maintain the altered phenotype even when vegetatively propagated.

13. EXAMPLE: BIOMASS PRODUCTION OF TRANSGENIC PLANTS EXPRESSING *cbd*

[0205] Tobacco F₁ plants of p35SC1 (*cbd* expressed under 35S promoter) and control plants transformed with pBI121 (Clontech Inc., Palo Alto, California) were germinated on plates and grown for 4 weeks. The two specific phenotypes generated by *cbd* expressing transgenes (large leaves/normal hypocotyl and small leaves/long hypocotyl) and large and small seedlings of control plants

were selected and transferred to fresh medium and grown for additional 3-4 weeks in the growth room and then transferred to the green house for 3-4 weeks. Leaf area, wet and dry weight of the plants was measured.

The results indicate that *cbd*-transgenic plants produce significantly more biomass as compare to the control plants (FIG. 15). Similar results were obtained with F₁ tobacco plants transformed with pCCI (CBD expression controlled by the *cel1* promoter) (FIG. 16).

14. EXAMPLE: *cel1* PROMOTER EXPRESSION IN ASPEN (*POPULUS TREMULA*)

14.1. MATERIALS AND METHODS

14.1.1. CONSTRUCTION OF TRANSGENIC PLANTS EXPRESSING *cel1* PROMOTER-gus FUSION

[0206] The 1.6 kb *cel1* promoter region (nucleotides 5-1618 of accession #X98543 (SEQ ID NO:9)) was cloned into the binary vector pBI101.1 at the 5' end of the β -glucuronidase *gus* gene. The construct was mobilized into disarmed Era101 *Agrobacterium tumefaciens* by triparental mating (An, 1987, Meth. Enzymol. 153:292-305). The transformation was performed with stem explants of *Populus tremula* (Tzfira et al., 1997, Physiologia Plantarum 99:554-561). Regenerated transgenic plants were selected on kanamycin. Eleven plants that were independently transformed with the construct were tested. The plants were analyzed for the presence of the *cel1* promoter region by Southern blot analysis. Transgenic poplar plants were grown in the growth chamber at 25°C under a 16hr photoperiod.

14.1.2. HISTOLOGICAL GUS STAINING ANALYSIS OF TRANSGENIC PLANTS

[0207] GUS staining was performed with X-Gluc as previously described (Jefferson et al., 1987, EMBO J. 6:3901-3907). Thirty day old seedlings were incubated overnight with X-Gluc at 37°C and then kept in a 70% ethanol solution prior to taking a photograph.

14.2. Results

[0208] The GUS staining indicated specific expression of the *cel1* promoter in fast growing tissues such as young leaves and the elongation zone of the stem as shown in FIGS. 17 and 18. The blue staining pattern correlated with the natural growth pattern of the cells in the developing leaves as shown in FIG. 19.

[0209] These results together with the results presented in Examples 11 and 17 show the *cel1* promoter directs tissue specific expression of GUS in growing organs of different transgenic plants such as Poplar, tobacco (see Example 11, *supra*) and *Arabidopsis* (see Example 17, *infra*).

15. EXAMPLE: EXPRESSION OF *cbd* IN POPLAR

[0210] Poplar plants expressing *cbd* under the CaMV 35S promoter showed a distinct phenotype (FIG. 20). The plants had shorter stature but with larger leaves compared to the control plants (FIG. 21). The roots appeared significantly thicker and were covered with many more root hairs that were more dense and longer than the control plants (FIGS. 22-24). Calcofluor staining showed that these plants accumulated cellulose at the tip zone of many of the root hairs indicating that *cbd* increased the rate of synthesis of the cellulose (FIGS. 25-28). This observation is in agreement with the *in vitro* experiments that showed that *cbd* accelerates the rate of synthesis of cellulose as shown in FIG. 30.

16. EXAMPLE: TRANSGENIC POPLAR PLANTS EXPRESSING *cel1*

[0211] Six independent transgenic poplar plants (out of 10) expressing *cel1* under the CaMV 35S promoter showed a distinct phenotype (FIG. 29). These plants appear to be larger compared to the control plants (transformed with the vector containing *gus* under the CAMV 35S promoter).

17. EXAMPLE: *cel1* EXPRESSION IN *ARABIDOPSIS*

[0212] The cDNA of *cel1* was cloned into the *E. coli* expression vector pET3d (Novagen, Madison, Wisconsin). The recombinant protein was used to produce polyclonal antibodies in rabbits. The specific antibodies reacted with a 65 kD protein. This protein was detected only in fast growing organs and was not found in old or fully developed tissues (FIG. 30).

18. EXAMPLE: THE EFFECT OF CBD ON CELLULOSE SYNTHESIS IN *ACETOBACTER XYLINUM*

18.1. INTRODUCTION

[0213] The gram-negative bacterium *Acetobacter xylinum* has long been regarded as a model of cellulose synthesis because cellulose microfibril synthesis is separated from cell wall formation (Ross et al. 1991, Microbiological Reviews 55:35-58). Since polymerization and crystallization are coupled processes in *A. xylinum* cellulose synthesis, interference with the crystallization results in an acceleration of polymerization (Benziman et al. 1980, Proc. Natl. Acad. Sci. USA 77:6678-6682). Some cellulose-binding organic substances can also alter cell growth and cellulose-microfibril assembly *in vivo*. For example, direct dyes, carboxymethyl cellulose (CMC) and fluorescent brightening agents (FBAs, e.g., calcofluor white ST) bind to the polysaccharide chains immediately after their extrusion from the cell surface, preventing normal assembly of microfibrils and cell walls. These molecules prevent microfibril crystallization, and

therefore enhance polymerization. (Haigler, 1991, "Relationship between polymerization and crystallization in microfibril biogenesis," in: Biosynthesis and Biodegradation of cellulose, pp. 99-124, eds C.H. Haigler and P.J. Weimer, Marcel Dekker, Inc., New York).

[0214] This experiment was conducted to determine the effects of *cbd* expression on cellulose synthesis.

18.2. MATERIAL AND METHODS

[0215] *Aectobacter xylinum* strain ATCC 23769 was used. Cells were grown for 24 hr in constant shaking at 30°C in a medium consisting of 0.5% Bactopeptone, 0.5% Yeast extract, 2% glucose and 0.3% K₂HPO₄ pH 6, and 1.5 Unit/ml *Trichoderma viride* cellulase (Fluka, Buchs, Switzerland). The cells were harvested by centrifugation and washed twice with pre-cooled phosphate buffer (50 mM NaH₂PO₄ pH 6). The bacterial pellet was resuspended in phosphate buffer to a concentration of 2 mg/ml dry weight (2.5 O.D₆₀₀=1 mg/ml). One ml of each of the reaction mixtures was placed in 20 ml scintillation vials containing 0.8 mg cells/ml phosphate buffer. Cellulose synthesis was initiated by the addition of 40 mM glucose (D-[U¹⁴C] glucose (Amersham, England) at a specific activity of 40,000 cpm/μmol and allowed to occur for 1-2 hr at 30°C with constant shaking. The ¹⁴CO₂ formed was trapped in coverless Ependorf tubes containing 0.2 ml 1 M NaOH placed in the reactions vial. The reaction was stopped by the addition of 0.1 ml of 0.5 M HCl to the bacterial suspension and incubated for 15 min. One hundred and fifty μl of the NaOH solution containing the trapped ¹⁴CO₂ were transferred to scintillation tubes. The cells and the cellulose were transferred to 1.5 ml Ependorf tubes, centrifuged and washed three times with water. The cells were lysed by mixing with 0.2 N NaOH, 1% SDS. Cellulose was recovered on GF/A filter (Whatman, Shrewsbury, MA) washed with 15 ml of water and dried in an oven at 60°C. Filters and NaOH containing trapped ¹⁴CO₂ were counted in a scintillation counter using "OPTI-FLUOR" (Packard) scintillation liquid to measure glucose incorporation (cellulose synthase activity) and respiration.

[0216] Electron microscopy was conducted by placing a drop of the appropriate solution on top of a copper grid at room temperature. The cellulose synthesis reaction contained 0.5 mg/ml dry weight cells in phosphate buffer, 40 mM glucose with or without CBD at a concentration of 300 μg/ml. The reaction was incubated for 30 min and then stopped with 2.5% glutardialdehyde (Merck, Rahway, New Jersey) for 30 min, washed three times with water and dried. The grids were negatively stained with 1.5% phosphotungstic acid and examined with a Jeol 100 CX electron microscope operating at 80 kV.

18.3. RESULTS

[0217] Resting cells of *Aectobacter xylinum* were allowed to synthesize cellulose in phosphate buffer con-

taining radioactive glucose and different concentrations of cbd or calcofluor (as a positive control) and BSA (as a negative control) for 1 hr or for the indicated length of time. Cellulose synthase activity was determined by the amount of glucose incorporated. FIG. 30 shows the effect of cbd at different concentrations (10 - 500 $\mu\text{g/ml}$, 0.6 - 30 μM) compared with 1 mM calcofluor and 100 $\mu\text{g/ml}$ BSA (1.5 μM). The cbd increased glucose incorporation in a dose responsive manner by up to five-fold at 500 $\mu\text{g/ml}$. Calcofluor increased the rate by two-fold while BSA had no effect. The rate of glucose oxidation to CO_2 was only marginally affected. Thus, glucose incorporation could be attributed to cellulose synthesis.

[0218] Electron microscopy examination of the cellulose ribbons produced by *A. xylinum* showed that CBD treatment resulted in a splayed ribbon composed of separate fibrillar subunits as compared with a thin and uniform ribbon in the control as shown in FIG. 31.

[0219] This example demonstrates, using the model system (*Acetobacter xylinum*), that cbd enhances cellulose synthase activity, comparable with the effect of the fluorescent brightening agent calcofluorwhite. The effect of cbd on cellulose synthase activity was dose-responsive with an optimum response around 10 mg/ml.

1.8.4. DISCUSSION

[0220] It is evident that polymerization and crystallization are coupled reactions in cellulose synthesis in *Acetobacter xylinum* bacteria (Benziman et al., 1980 Proc. Natl. Acad. Sci. USA 77:6678-6682). Addition of cbd to the culture medium enhanced the incorporation of radioactive glucose in *A. xylinum*. While not intending to be limited to any particular mechanism of action on cellulose synthesis, the present inventors believe that cbd enhanced incorporation of radioactive glucose by interfering with the cellulose crystallization process. Our hypothesis is supported by Haigler's review (1991, "Relationship between polymerization and crystallization in microfibril biogenesis," in: Biosynthesis and Biodegradation of Cellulose, pp. 99-124, eds Haigler and Weimer, Marcel Dekker, Inc., New York), in which dyes and fluorescent brightening agents that bind to cellulose were shown to alter cellulose microfibril assembly *in vivo*. Modifications in cell shape were observed when red alga (Waaland and Waaland, 1975, Planta 126:127-138) and root tips (Hughes and McCully, 1975, EMBO J. 6:3901-3907) were grown in the presence of dyes. It is now evident that these molecules can bind to the cellulose chains immediately upon their extrusion from the cell surface of prokaryotes and eukaryotes (Haigler and Brown, 1979, J. cell Biol. 83, 70a; Benziman et al., 1980, Proc. Natl. Acad. Sci. USA 77:6678-6682; Haigler et al., 1980, Science 210:903-906; Brown et al., 1982, Science 218:1141-1142) and prevent crystal-structure formation (Haigler and Chanzy, 1988, J. Ultrastruct. Mol. Struct. Res. 98:299-311). In addition, the rate of cellulose polymerization was shown to increase up to fourfold in the

presence of dye (Benziman et al., 1980, Proc. Natl. Acad. Sci. USA 77:6678-6682). Crystallization was proposed to be the bottleneck in this coupled reaction and its prevention to result in accelerated polymerization. The effect of cbd as observed by electron microscopy is comparable to the effect of CMC (carboxy methyl cellulose) rather than to the effect of calcofluor (Haigler, 1991, "Relationship between polymerization and crystallization in microfibril biogenesis," in Biosynthesis and Biodegradation of Cellulose, pp. 99-124, eds Haigler and Weimer, Marcel Dekker, Inc., New York) in both cases the cellulose ribbon only splayed. The effect of cbd on cellulose synthase activity was higher than the effect of CMC and was comparable to and even higher than that of calcofluor (FIG. 31). The different effects of cbd, CMC and calcofluor can be attributed to the differences in the molecular weights and the affinities to cellulose. CMC (90 kDa) can only prevent the normal association of larger fibrillar subunits and, therefore, hardly alters crystallization, while the small molecule calcofluor prevents the glucan chain association immediately after its initiation. The size of the cbd is somewhere in between that of calcofluor and CMC. On one hand, it is not small enough to prevent association of very small fibrils as achieved by calcofluor, but on the other hand, its high affinity to cellulose makes it an efficient cellulose intercalating agent which leads to an increase in the rate of cellulose synthesis of up to fivefold.

[0221] Based on results presented above, transgenic plants, such as alfalfa for example, expressing any CBD, including but not limited to cbd, will not only have higher level of biomass, but also have cellulose more amenable for degradation by ruminants and, therefore, have a higher nutritional value than normal non-transgenic plants.

19. EXAMPLE: MODIFICATION OF PLANT CELL WALL AND MECHANICAL STRENGTH OF TRANSGENIC PLANTS EXPRESSING *cbd*

[0222] Stems of poplar plants expressing *cbd* under the CaMV 35S promoter and control plants (transformed with the vector containing *gus* (in place of *cbd*) under the CaMV 35S promoter) were imbedded in paraffin. Cross sections were stained with CIZnI (FIGS. 33A-D). Stems of plants expressing *cbd* appear to have thicker cell walls. The stems were physically stronger as they maintained their structure while control stems were crushed under the same sectioning process.

[0223] Calcofluor staining of the roots (FIGS. 34A-B) indicated that roots of plants expressing *cbd* appear to have thicker cell walls. The roots were physically stronger as they maintained their structure while control stems were crushed under the same sectioning process.

[0224] These results indicate that expression of *cbd* in plants can improve the ability of plants to withstand physical and environmental biotic and abiotic stresses.

20. EXAMPLE: MODIFICATION OF PLANT POLYSACCHARIDES IN PLANTS EXPRESSING *cbd*

[0225] It was noted that cells of poplar plants expressing *cbd* accumulated dark granules that were scarce or absent in control plants. See FIGS. 33B and D vs. A and C for stem cells and FIG. 35A vs. B for root cells. Poplar stems expressing *cbd* and control plants (transformed with the vector containing *gus* under the CaMV 35S promoter) were stained with IKI which specifically stains starch (FIGS. 36A and B). Potato tuber sections were also stained with IKI as a positive control. The results indicated that the dark granules are made of starch.

[0226] One possible explanation of the mechanism for the accumulation of starch in plants expressing *cbd*, and in no way a limitation of the present invention, is that sucrose is proposed to be the transported sugar and the major metabolite in plant cell wall biosynthesis. Sucrose synthase utilizes sucrose and UDP to make UDP-glucose and fructose. UDP-glucose serves as the substrate of cellulose synthase. The accumulated fructose may be converted in several steps to starch utilizing for example, fructokinase to give fructose-6-P, glucose-phosphate-isomerase to give glucose-6-P, phosphoglucomutase to give glucose-1-P, ADPG-pyrophosphorylase to give ADP-glucose which is the substrate of starch synthase. Expressing *cbd* in plants affects general polysaccharide distribution and, therefore, affects the nutritional value of different crops.

21. EXAMPLE: GROWTH STIMULATION

[0227] Expression of *cbd* in tobacco plants was tested using two promoters (CaMV 358 promoter and *A. thaliana cel1* promoter). Plants expressing *cbd* under either promoter, grew faster than control plants and started to bloom significantly before control plants (FIG. 37). Expression of *cbd* in plants appears to shorten the time for harvest of crops.

22. EXAMPLE: TRANSGENIC PLANTS EXPRESSING *Cell* EFFECT ON PLANT HEIGHT AND FIBER LENGTH

[0228] Individual transgenic poplar plants expressing *cel1* under the CaMV 35S promoter were micropropagated and grown *in vitro*. The plants were taller as compared to the control plants (transformed with the vector containing *gus* under the CaMV 35S promoter). The mean internode length of the plants expressing *cel1* was significantly higher than the control (FIG. 38).

[0229] The mean length of fiber cells of two transgenic plants expressing *cel1* (Cell. 5 and Cell. 18), was compared to that of the wild type (FIG. 39). The length of the fiber cells of the transgenic plants were significantly higher.

[0230] The length of the fiber cells could affect the mechanical properties of transgenic plants expressing *Cell*.

23. EXAMPLE: NORTHERN BLOT ANALYSIS OF TRANSGENIC POPLAR PLANTS

[0231] This example shows the results of a Northern blot analysis of RNA from controls plants and transgenic poplar plants which confirm the expression of the *cbd* gene (FIG. 40, lane 1 represents control wild type and lane 2 transgenic plant). The Northern blots were conducted as described in Example 6.7.

24. EXAMPLE: TRANSGENIC PLANTS HAVING IMPROVED HEAT RESISTANCE

[0232] Transgenic poplar plants expressing *cbd* under the CaMV 35S promoter; control plants (transformed with the vector combining *gus* (in place of *cbd*) under the CaMV 35S promoter); and wild type plants were transferred from an environmentally controlled growth room maintained at 25°C to a greenhouse where temperatures ranged from 32-38°C. The following days the plants were scored for the percentage of healthy remaining plants, wilted or dead plants. The data presented in Table 1 show that the *cbd* transgenic plants have improved resistance to heat compared to wild type and control plants.

Table 1

	% Healthy	% Dead	% Wilted
<i>cbd</i>	77	15	8
wild type	25	33	42
control	35	13	52

25. DEPOSIT OF PLASMIDS

[0233] The following plasmids were deposited with the American Type Culture Collection (ATCC), 10801 University Boulevard, Manassas, VA on January 12, 1998, and have been assigned the indicated accession numbers:

Plasmid	Accession Number
pPS	209577
pCEL1	209576

[0234] Although the invention is described in detail with reference to specific embodiments thereof, it will be understood that variations which are functionally equivalent are within the scope of this invention. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims.

[0235] Various publications are cited herein.

Claims

1. A transgenic plant having a nucleic acid construct comprising a nucleic acid encoding a cell wall modulation protein or polypeptide operably linked to a promoter so that the cell wall modulation protein or polypeptide is expressed and secreted from the transgenic plant cell, said transgenic plant has a higher biomass or faster growth rate compared to a progenitor plant which does not contain the construct when the transgenic plant and progenitor plant are cultivated under the same conditions, wherein said cell wall modulation protein or polypeptide is an endo-1,4-beta-glucanase.
2. The transgenic plant of claim 1, wherein said endo-1,4-beta-glucanase is Cel1 obtainable from *Arabidopsis thaliana*.
3. The transgenic plant of claim 1 or 2, wherein said nucleic acid encoding a cell wall modulation protein or polypeptide is fused to a nucleic acid sequence encoding a secretion signal peptide.
4. The transgenic plant of claim 1 or 2, wherein the promoter is a *cel1* functional promoter.
5. A seed of the transgenic plant of claim 1, wherein the seed has the recombinant nucleic acid construct.

Patentansprüche

1. Transgene Pflanze, die ein Nukleinsäurekonstrukt aufweist, welches eine Nukleinsäure umfasst, die ein funktionell mit einem Promoter verknüpftes Zellwandmodulationsprotein oder -polypeptid kodiert, sodass das Zellwandmodulationsprotein oder -polypeptid exprimiert und aus der transgenen Pflanzenzelle sezerniert wird, wobei die transgene Pflanze im Vergleich zu einer das Konstrukt nicht enthaltenden Vorläuferpflanze eine höhere Biomasse oder schnellere Wachstumsrate aufweist, wenn die transgene Pflanze und die Vorläuferpflanze unter denselben Bedingungen gezüchtet werden, wobei das Zellwandmodulationsprotein oder -polypeptid eine Endo-1,4-beta-Glucanase ist.
2. Transgene Pflanze nach Anspruch 1, wobei die Endo-1,4-beta-Glucanase Cel1 ist, erhältlich aus *Arabidopsis thaliana*.
3. Transgene Pflanze nach Anspruch 1 oder 2, wobei die ein Zellwandmodulationsprotein oder -polypeptid kodierende Nukleinsäure an eine Nukleinsäuresequenz fusioniert ist, die ein Sekretionssignalpeptid kodiert.

4. Transgene Pflanze nach Anspruch 1 oder 2, wobei der Promoter ein funktioneller *cel1*-Promoter ist.
5. Samen der transgenen Pflanze nach Anspruch 1, wobei der Samen das rekombinante Nukleinsäurekonstrukt aufweist.

Revendications

1. Plante transgénique contenant une construction d'acide nucléique comprenant un acide nucléique codant pour une protéine ou un polypeptide de modulation de la paroi cellulaire fonctionnellement lié à un promoteur de telle façon que la protéine ou le polypeptide de modulation de la paroi cellulaire est exprimé et sécrété à partir de la cellule de plante transgénique, ladite plante transgénique présente une biomasse supérieure ou une vitesse de croissance plus rapide comparativement à une plante progéniteur qui ne contient pas la construction lorsque la plante transgénique et la plante progéniteur sont cultivées dans les mêmes conditions, où ladite protéine ou ledit polypeptide de modulation de la paroi cellulaire est une endo-1,4-bêta-glucanase.
2. Plante transgénique selon la revendication 1, où ladite endo-1,4-bêta-glucanase est Cell susceptible d'être obtenue à partir d'*Arabidopsis thaliana*.
3. Plante transgénique selon la revendication 1 ou 2, dans laquelle ledit acide nucléique codant pour une protéine ou un polypeptide de modulation de la paroi cellulaire est fusionné à une séquence d'acide nucléique codant pour un peptide signal de sécrétion.
4. Plante transgénique selon la revendication 1 ou 2, où le promoteur est un promoteur fonctionnel de *cel1*.
5. Graine de la plante transgénique selon la revendication 1, où la graine comporte la construction d'acide nucléique recombinant.

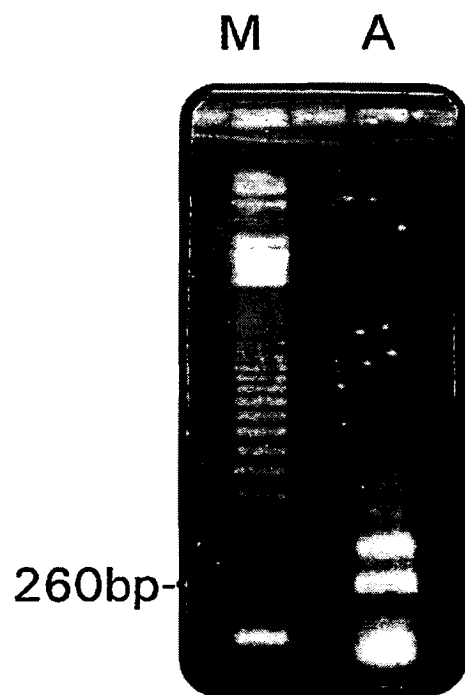


FIG.1

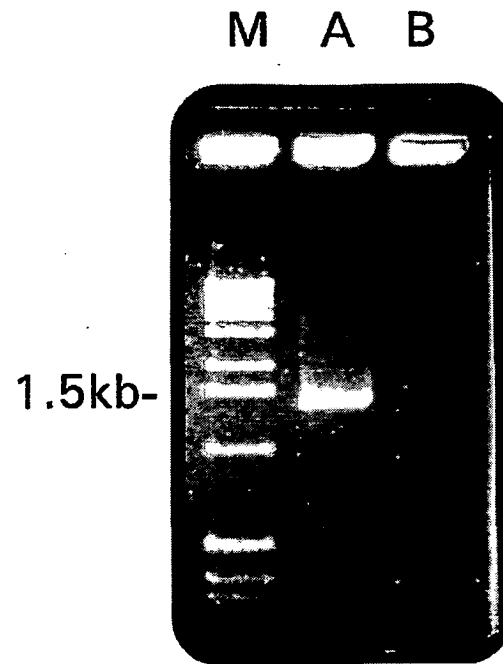


FIG.3

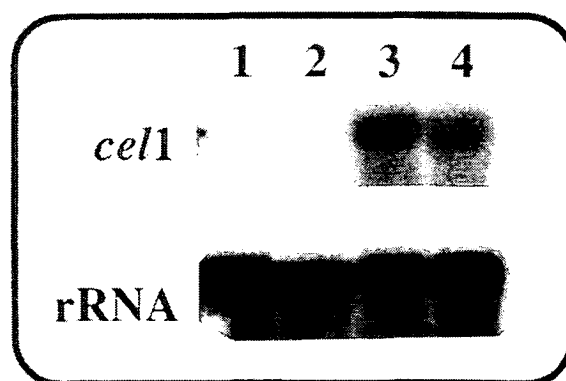


FIG.6

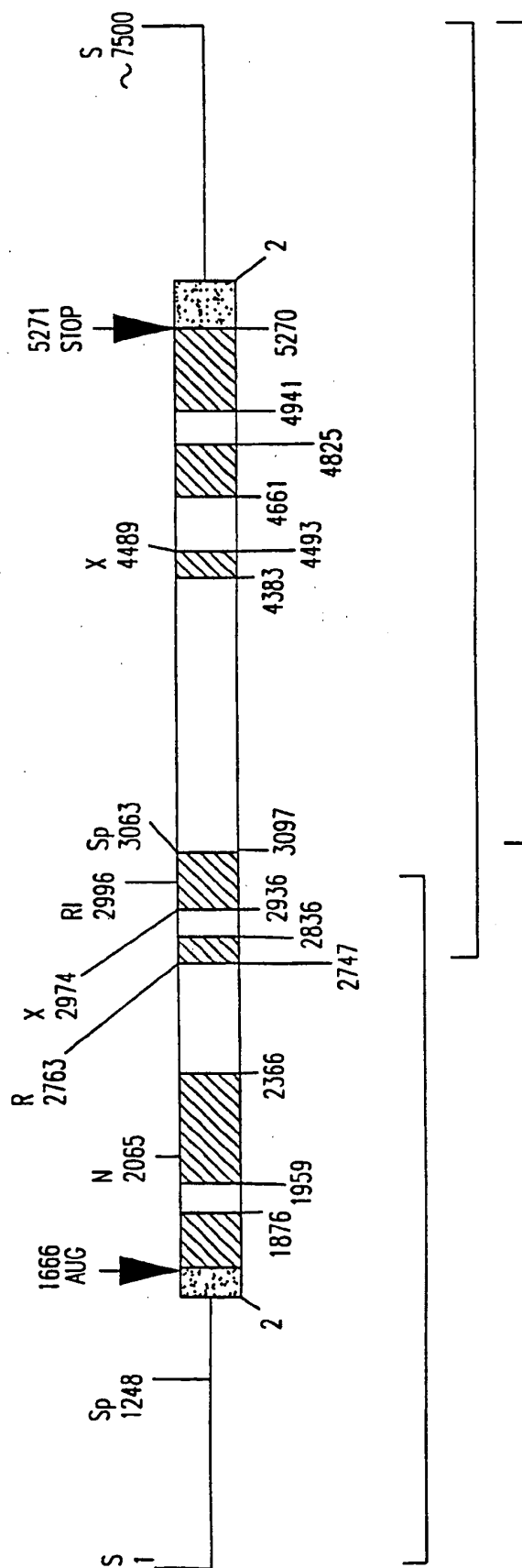


FIG.2

2	ARKSLIFPVILHAVLLFSPPIYSAGH.DYRDALRKSILFFEGQRSGKLPP	50
5	SPLSLFHLLL VCTVMV...KCCSASDLHYSDALEKSILFFEGQRSGKLPT	51
51	DQRLKWRRDSALRDGSSAGVDLSGGYYDAGDNIKFGFPMAF TTTMLSWSI	100
52	NQRLTWRGDSGLSDGSSYHVDLVGGYYDAGDNLKFGLPMAF TTTMLAWGI	101
101	IDFGKTMGP E LRNAVKAVKWGTDYLLKA.TAIPGVVFVQVGDAYSDHNCW	149
102	IEFGCLMPEQVENARAALRWSTDYLLKASTATSNSLYVQVGEPNADHRCW	151
150	ERPEDMDTLRTVYKIDRAHPGSDVAGETAALAAASIVFRKRDPAYSRL	199
152	ERPEDMDTPRNVYKVSTQNP GSDVAETAALAAASIVGSDSSYSTKL	201
200	LDRATR VF AFANRYRGAYSNSLYHADCPFYCDFNGYQDELLWGAAWLHKA	249
202	LHTAVKVF EFADQYRGYSDSLGSVVC PFYCSYSGYNDELLWGASWLHRA	251
250	SRKRAYREFIVKNEVILKAGDTINEFGWDNKHAGINVLISKEVLNCKAEY	299
252	SQNASYMTYIQSNGHTLGADDDYSFSWDDKRVGTVLLSKGFLQDRIEE	301
300	FESFKQNADGFICSLPGISHPQVQYSRGGLLVKTGGSNMQHVSLSFLL	349
302	LQLYKVHTDNYICSLIPGTSSFQAQYTPGGLLYKGSASNLQYVTSTAFLL	351
350	LAYSNYLSHAKKVPCGELTASPSLLRQIAKRQVDYILGDNPMGLSYMVG	399
352	LYYANYLNSSGGHASC GTTTVTAKNLSLAKKQVDYILGQNP AKMSYMVG	401
400	YGOKEPRRIHHRGSSVPSVSAHPSHIGCKEGSRYFLSPNPNPNLLVGAVV	449
402	FGERTPQHVHHRGSSLPSVQVHPNSIPCNAGFYLYSSPPNPNILVGAIL	451
450	GGPNVTD A FPD SRPYFQQSEPTTYINAPLVGLLG YFSAHST	490
452	GGPDNRDSFSDDRNNYQQSEPATYINAPLVGALAFFAANPV	492

FIG. 4

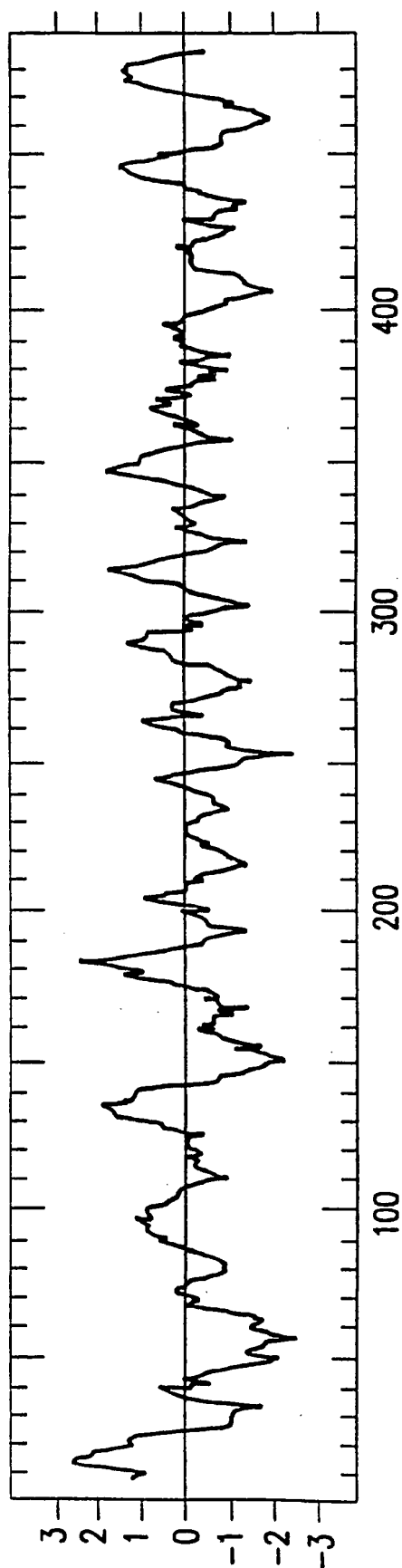


FIG. 5A

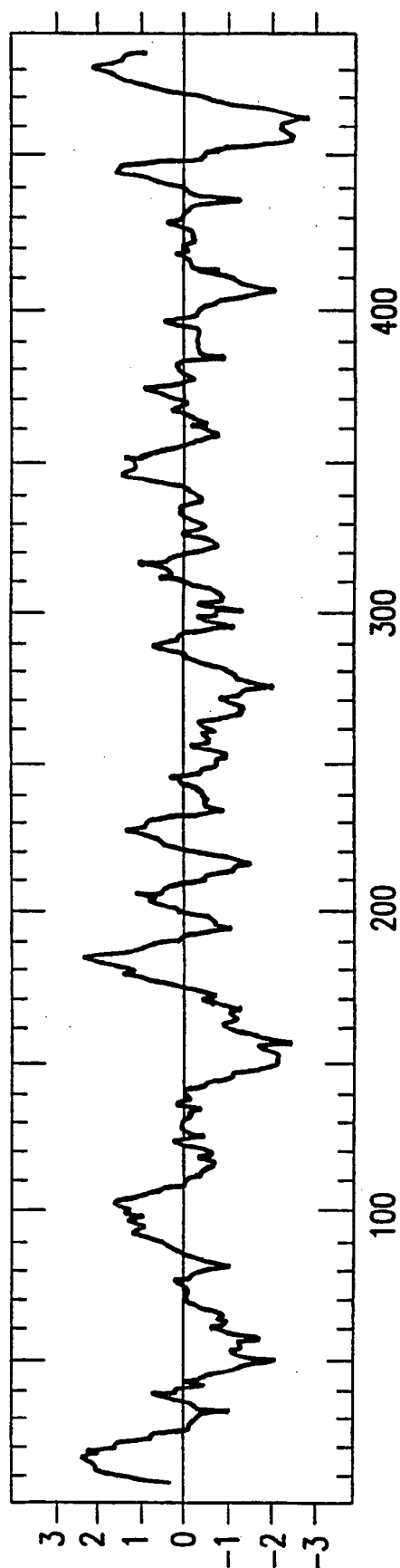


FIG. 5B

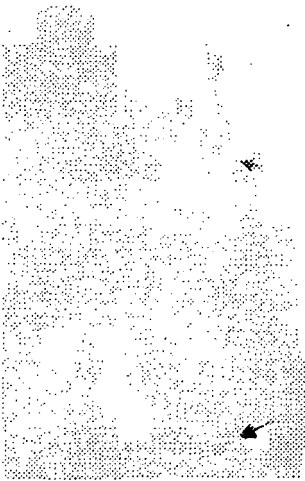


FIG. 7A

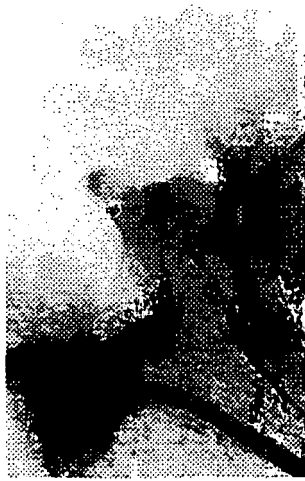


FIG. 7B



FIG. 7C

GTCGACCTGCAGGTCAACGGATCACATGCATCAGCACTATTTACAACAATCCTTTAGGGT	60
ATATGTTAGTCAACCCCGTAACACCATTCGTACCCATTAATCATGAACATTTGCGCAAAGT	120
TTTCCACCAAAAACGGCGTCGGATAAGGTTTTTGGCATTGTTTCTTTTTTTGTGT	180
GCATAGCATAATTTCAATTTAAACCGTACTATTGGAAGATTTTAAATTGGATAAAGATGA	240
TTCATTCAATACATAGTCGCTTTGTTGTTACTAGTGATAAATTCATGTTAATGATTCTAT	300
GATTTTCGGCCAGCTATCTCATTAATTATTAAGACGTTTAAGTGGAGCTATTAGCAATCG	360
TGTATGACATAATGATTAGCATTTTCATGTGCCATGCCCATGCATGAGGCTTTTTTTTTGT	420
TTAAAATTTTATTCTATTATATCCGAATTTTGTTATATACTAAATGAACATTTGTCTCTG	480
ATTTGGTCTACTAGTTAATTAACCTTTAGCTTCACTAATAAAAAATCTCATGATTTTGAT	540
ACTTAAACCCAAAACATATTA AAAACAATTAGCAGTCTTTTAAATCGATAATGTGCTTAG	600
ATGATTATACGTTCTAGGAACTCTTTTGTTTCCAATGCATGTTAAGAACTAAGAACTC	660
GTATCCTTAAGCACCAATGCTTTATGCTTAATGCCTCATTAGAGATATAAACTGAGATTG	720
ACTGTGTTCTGAATCATCATAATATAAGGCACACAAAGAACAGAACAGGAAATACTTAGC	780
AATATAATAGGTTTCCAATAAAAGTGAAGAAGAATACAATAAACTTTTATAAAAAAAAAA	840
GTATATAATAATTTCACTCGAATCAACCAAATGTAAGATGTCTTGTCCATTTACACAT	900
CACATGAGTAAGTGGATTACAGATTGCAATTGATGAAATCTGGATCTTAGCTAAAAATTT	960
ATTACGTTACTATATACATCGAGTTTTAAGATGTTTATAATCACAACCACAACCACAAGT	1020
TTGAAGAAATAAGAAACAGAGTAATAATATATCAAATAAAATTTTCATGGCTGATGGAATC	1080
TTTTTTCTAATTGTAGGTCCAAAAAAGCCTAAATTAATGGGGAAACAAAAACCAAATTC	1140
AATAGTAATTTTACTAATTATGTCTTGTTAAATAGAGTAAAAAGAAAATTAATCACAAA	1200
CCTCCAAAAATCACTAATTGAGATCAAAACACGTGTCGCATGCCAATAGGGCGGTGGAT	1260
CACATGGTAAAAAAATTCACCTTTAATTTTTGTCTTTCTTCATAATTCATCTCACAGATTT	1320
CAACTTCTCTTTTGATTCTCTCACCGTACACCGTCGGCGTACCACTCCCCTTCCACACC	1380
GTCGGTATTA AAAATCTCAAACCCTAAAACCCGTATCCAATAACCCACCCGGTCCAACCG	1440
GTTATTCAAACCCGGTCAATCCAAAATTCGCCTCGGAATCCAAACCTCCATACCCAATCT	1500
AACATGGAAAAACCTCCAATCACAAACCTCCACGTGGTGATCACTCATTGGCTCTTATTC	1560
TGGAATCCAAGAGGACCTTTTTAGTATAAAGAGCCCCTTCGTTGGTCCTATCACCTTCTC	1620
TCTCTCACACACTAACAGAAAGCACAGAAGAAGAGACAAAAGAATGGCGCGAAAATCC	1680
CTAATTTTCCCGGTGATTTTGCTCGCCGTTCTTCTCTCTCCGCGATTACTCCGCC	1740
GGTCACGATTACCGCGACGCTCTCCGTAAA	1770

FIG.8

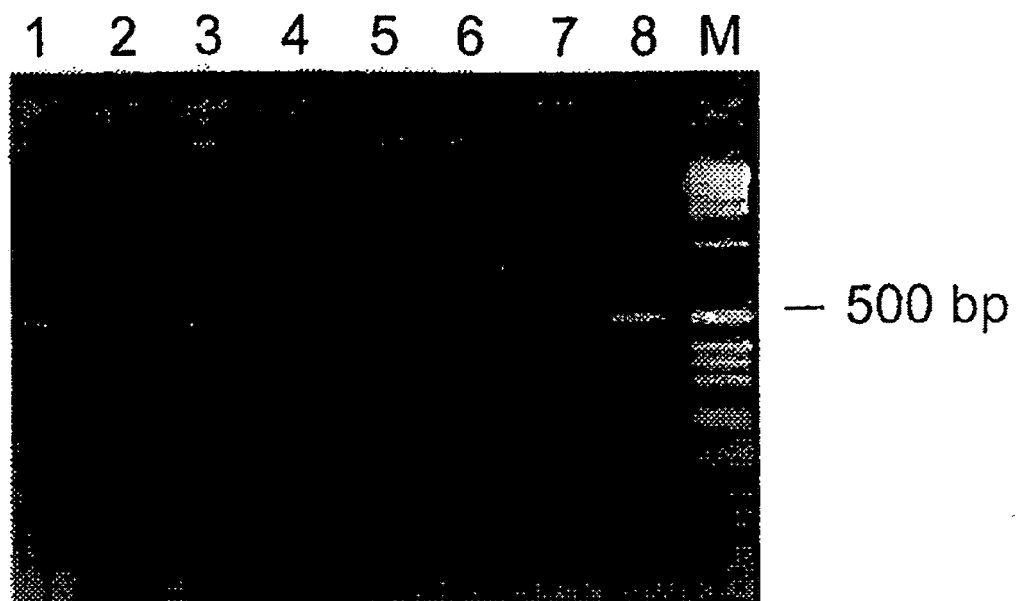


FIG. 9

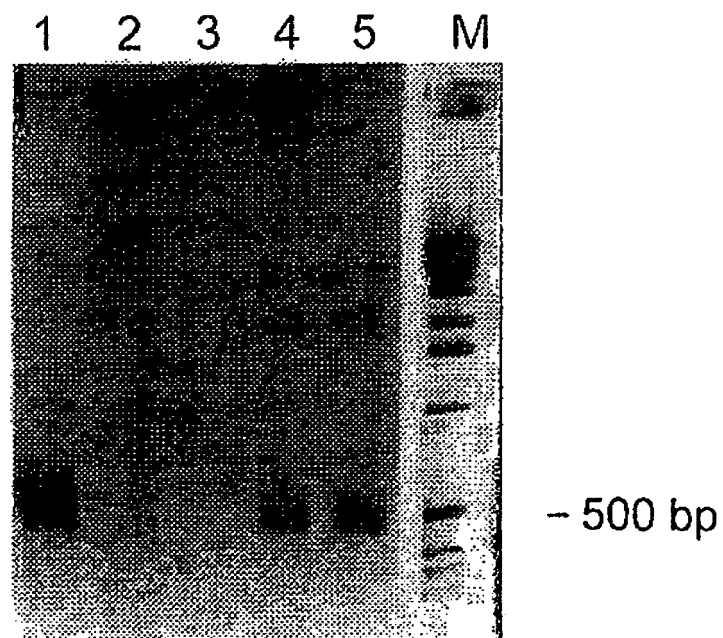


FIG.10

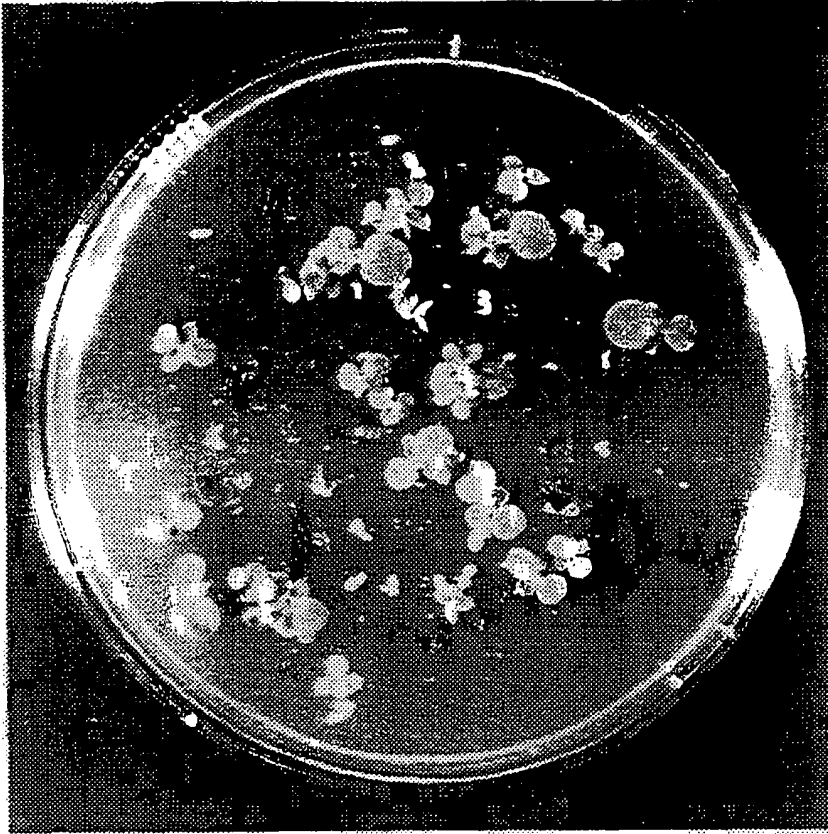


FIG. 11B

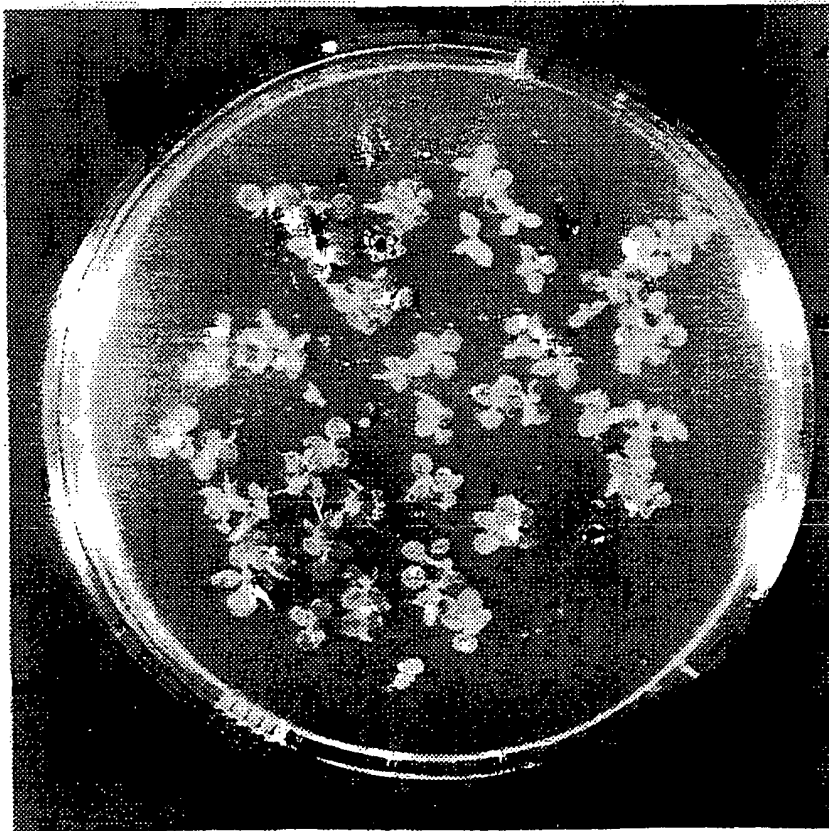


FIG. 11A



FIG. 12A



FIG. 12B

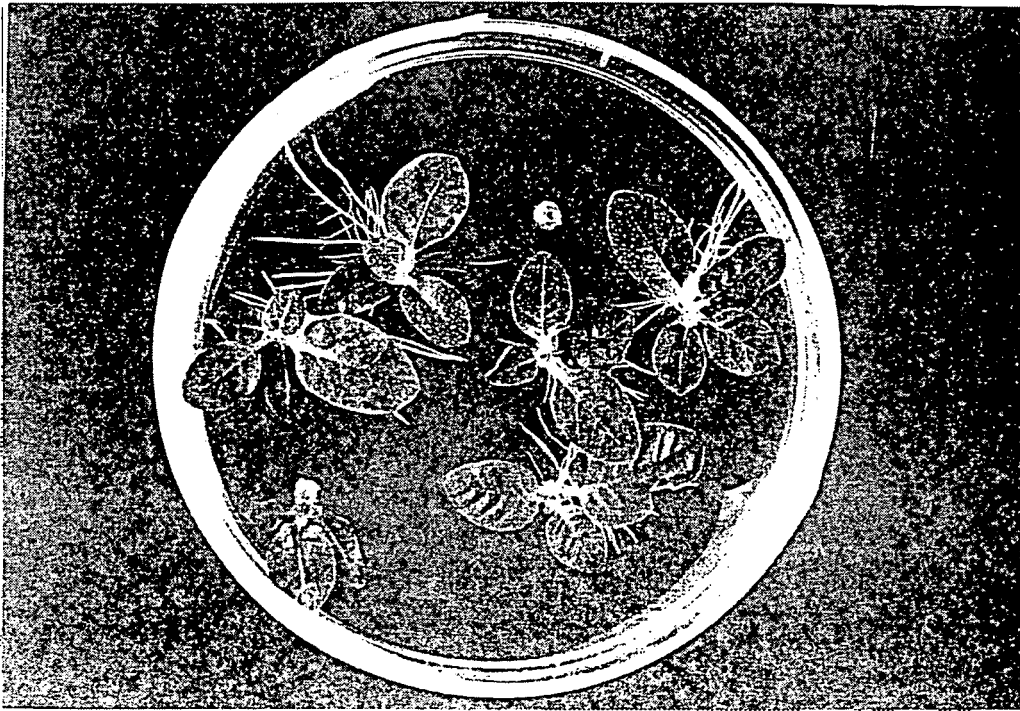


FIG. 13A

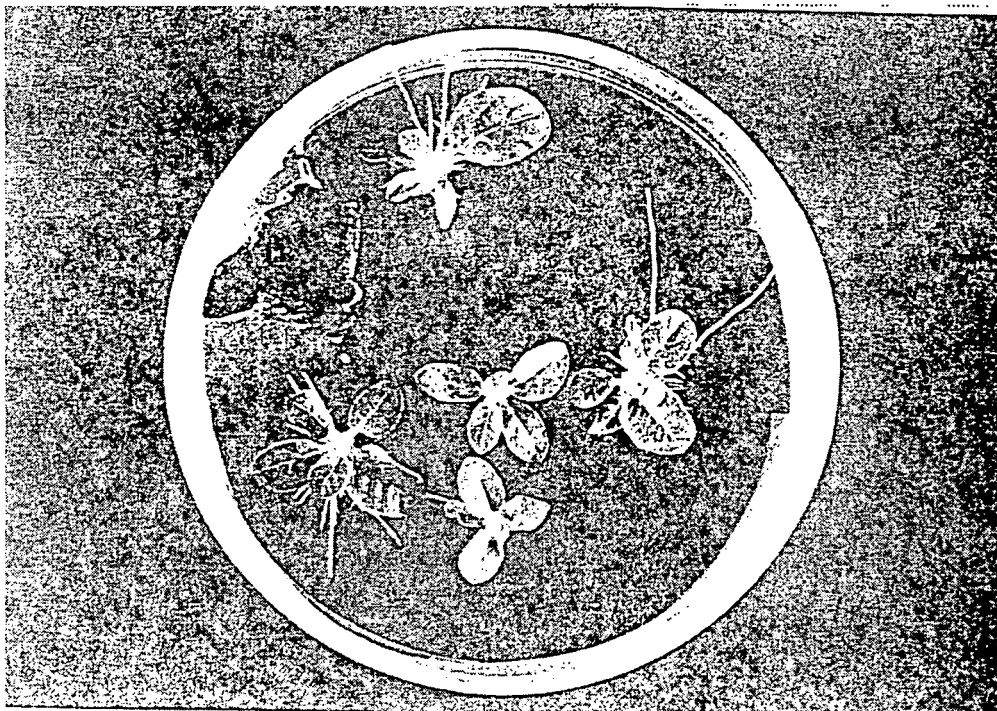


FIG. 13B

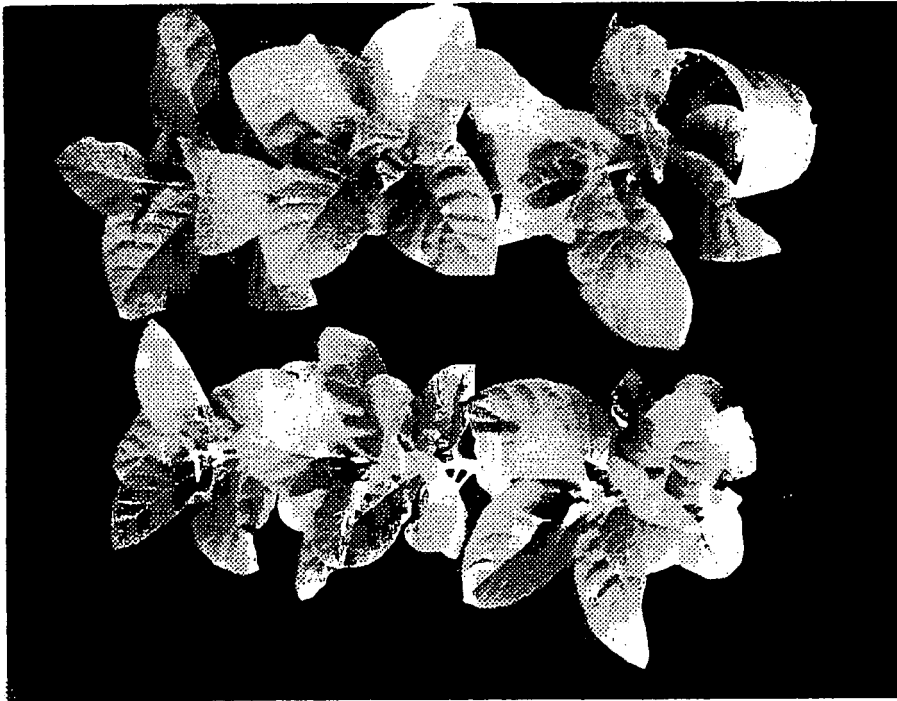


FIG. 14B

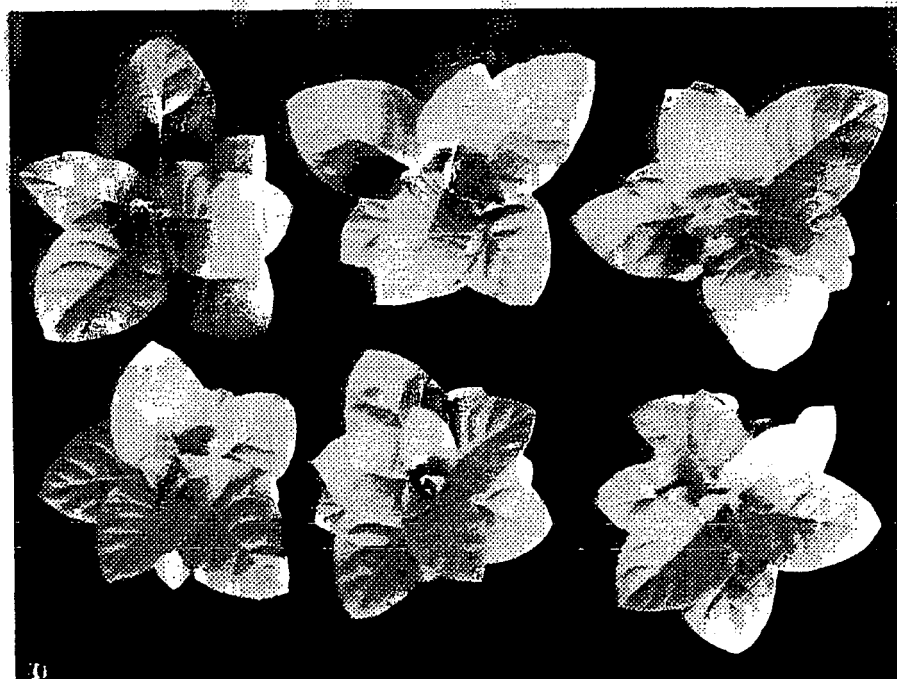


FIG. 14A

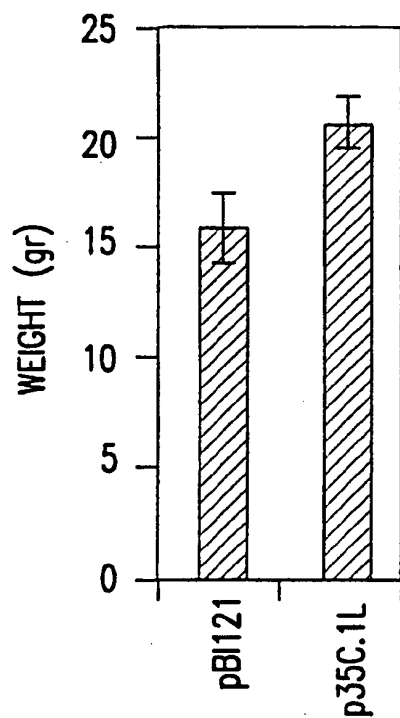


FIG.15A

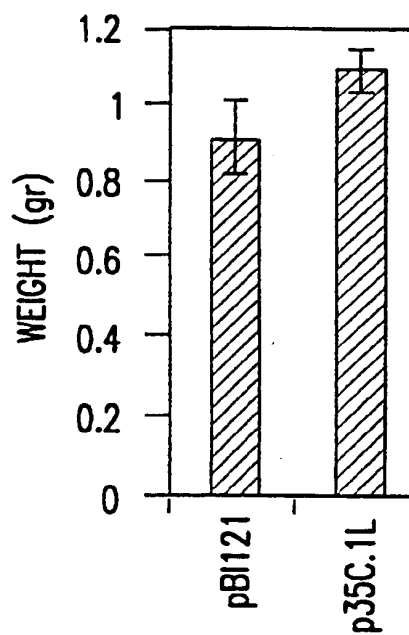


FIG.15B

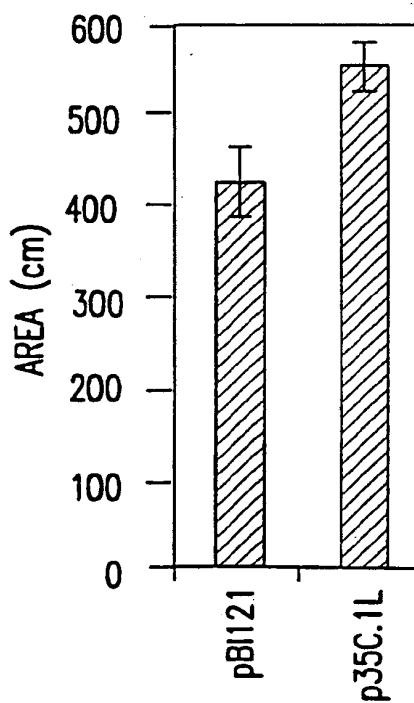


FIG.15C

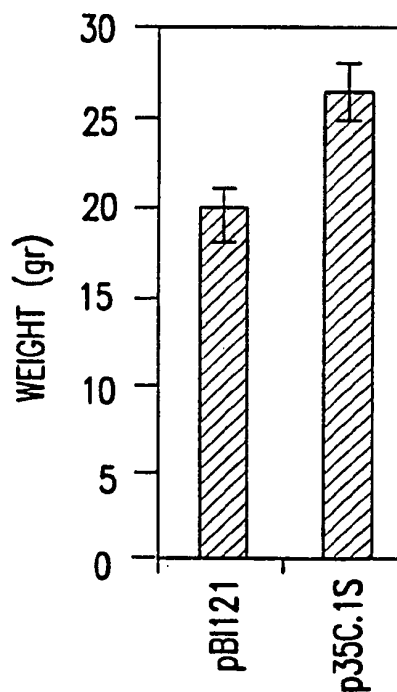


FIG.15D

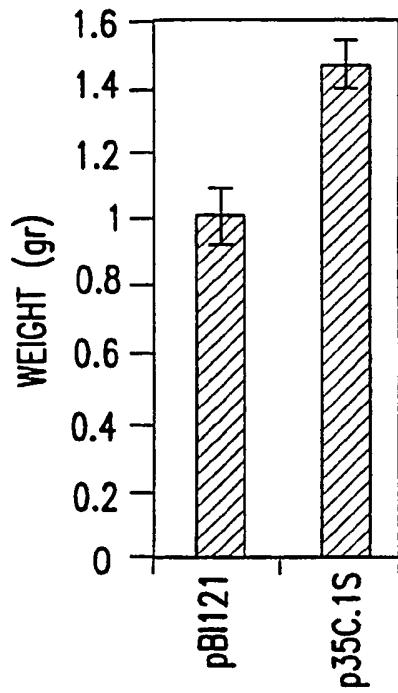


FIG.15E

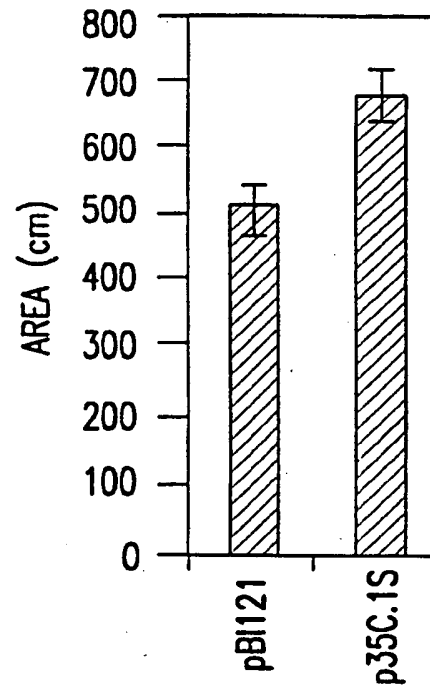


FIG.15F

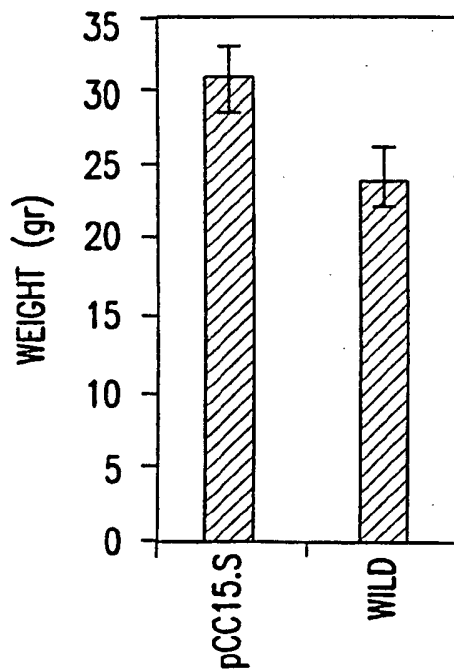


FIG.16A

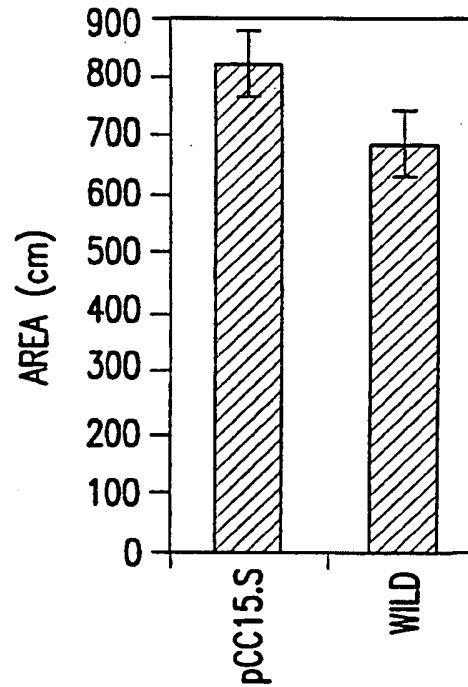


FIG.16B

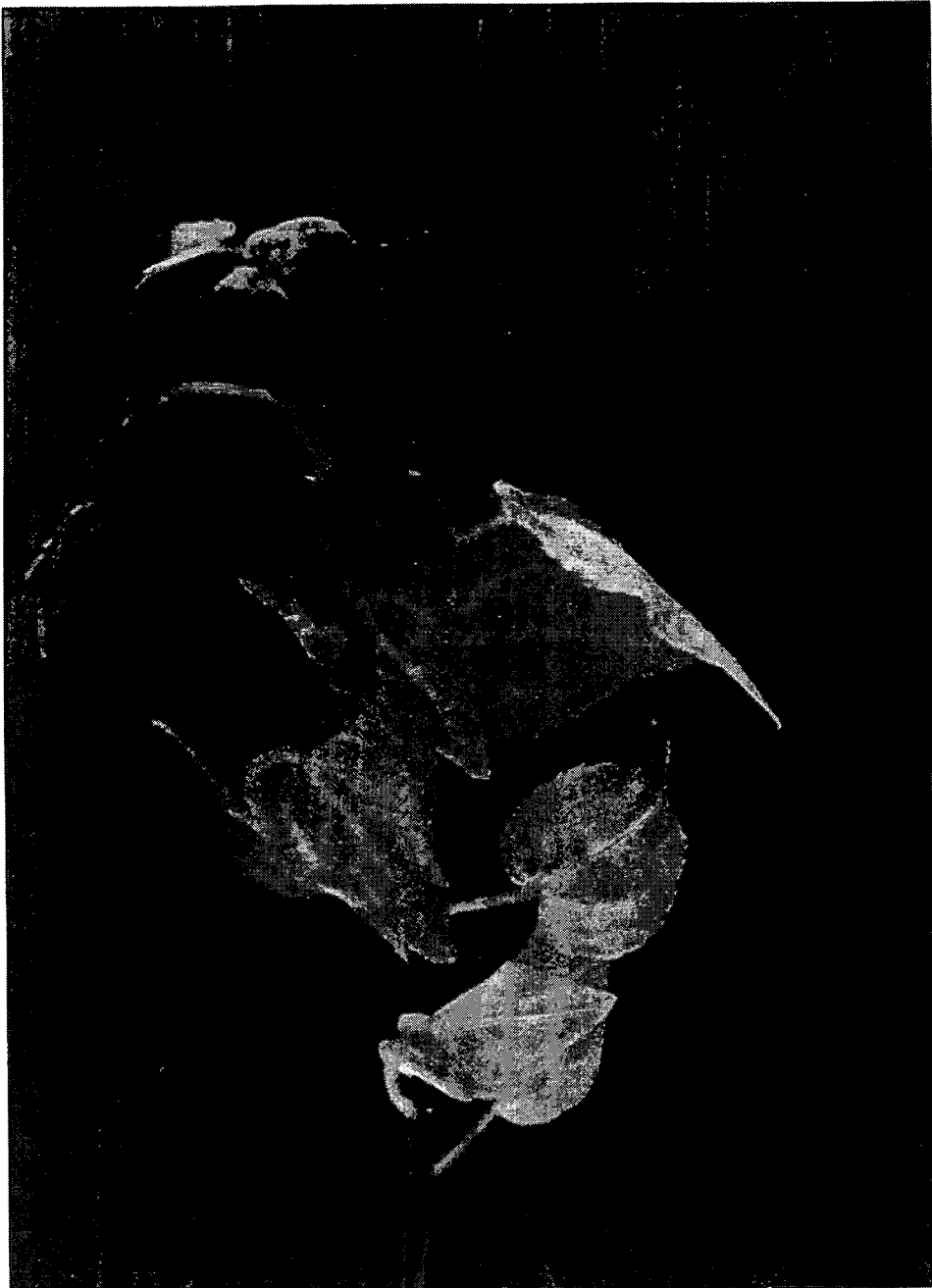


FIG.17

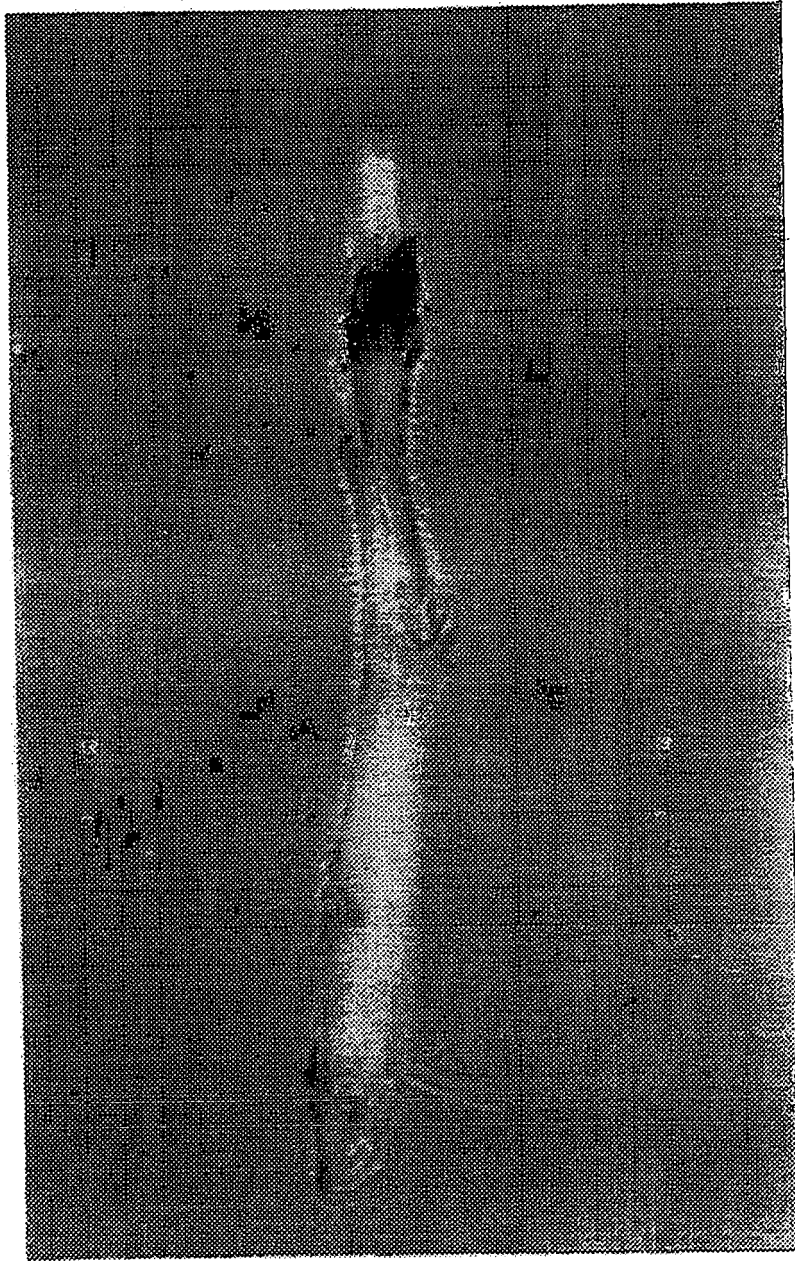


FIG.18



FIG. 19



FIG.20



FIG.21



FIG.22



FIG.23

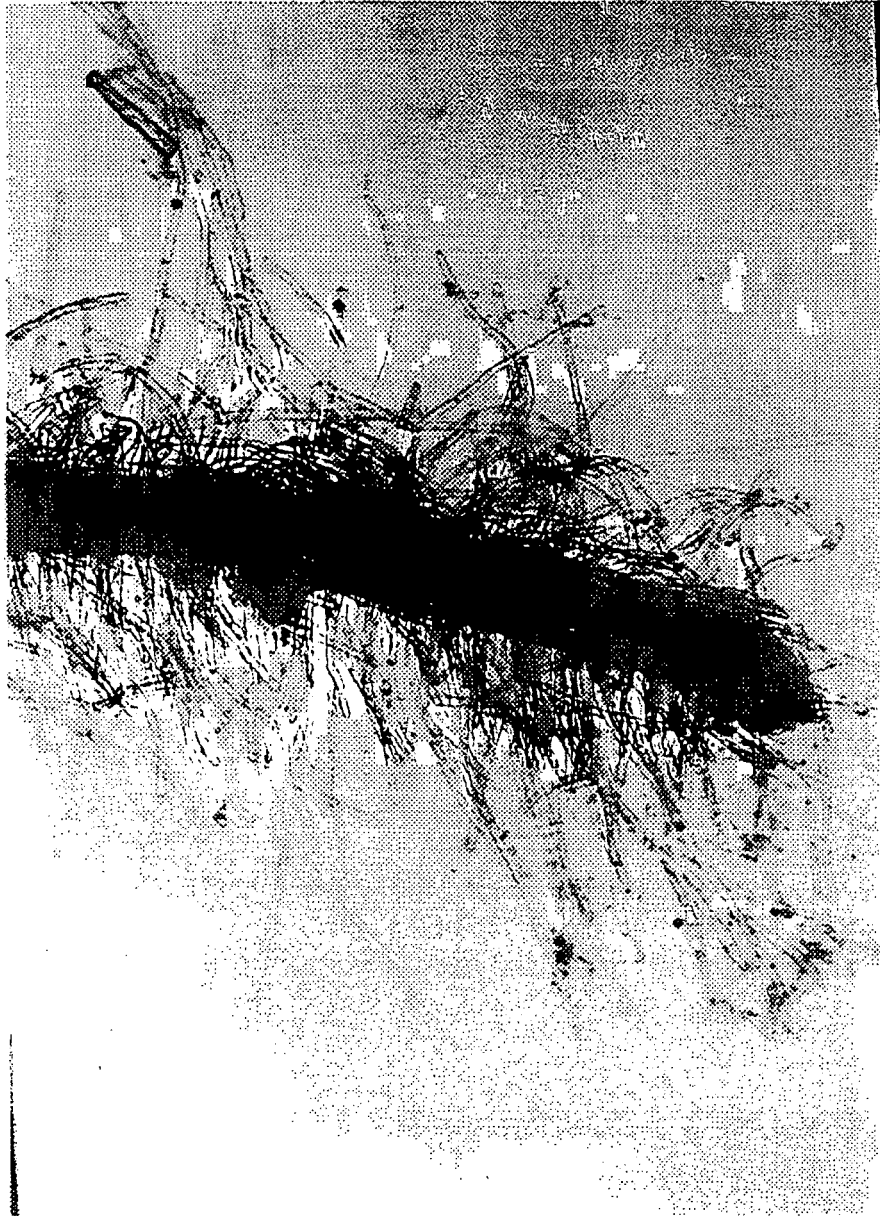


FIG.24

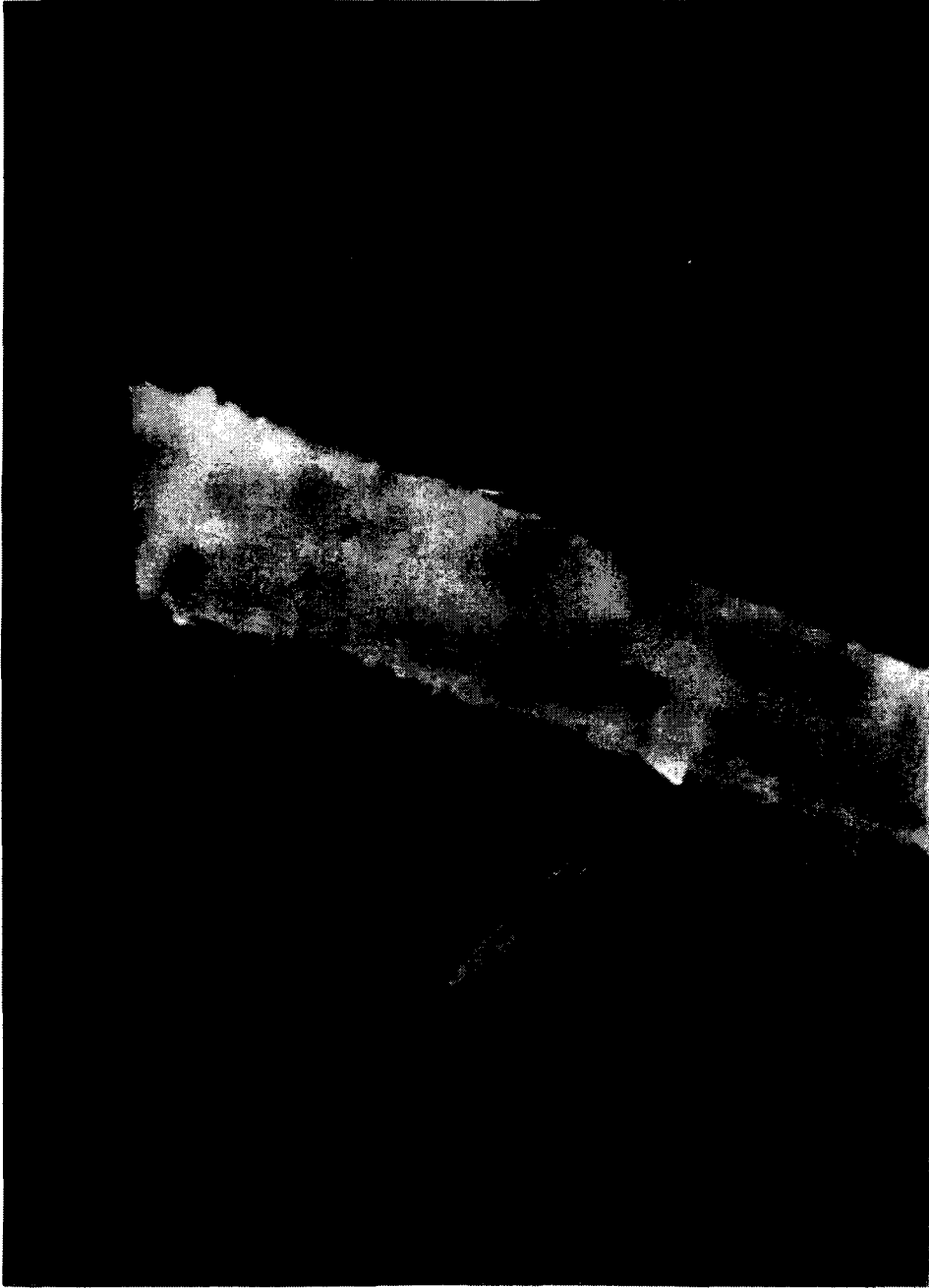


FIG. 25

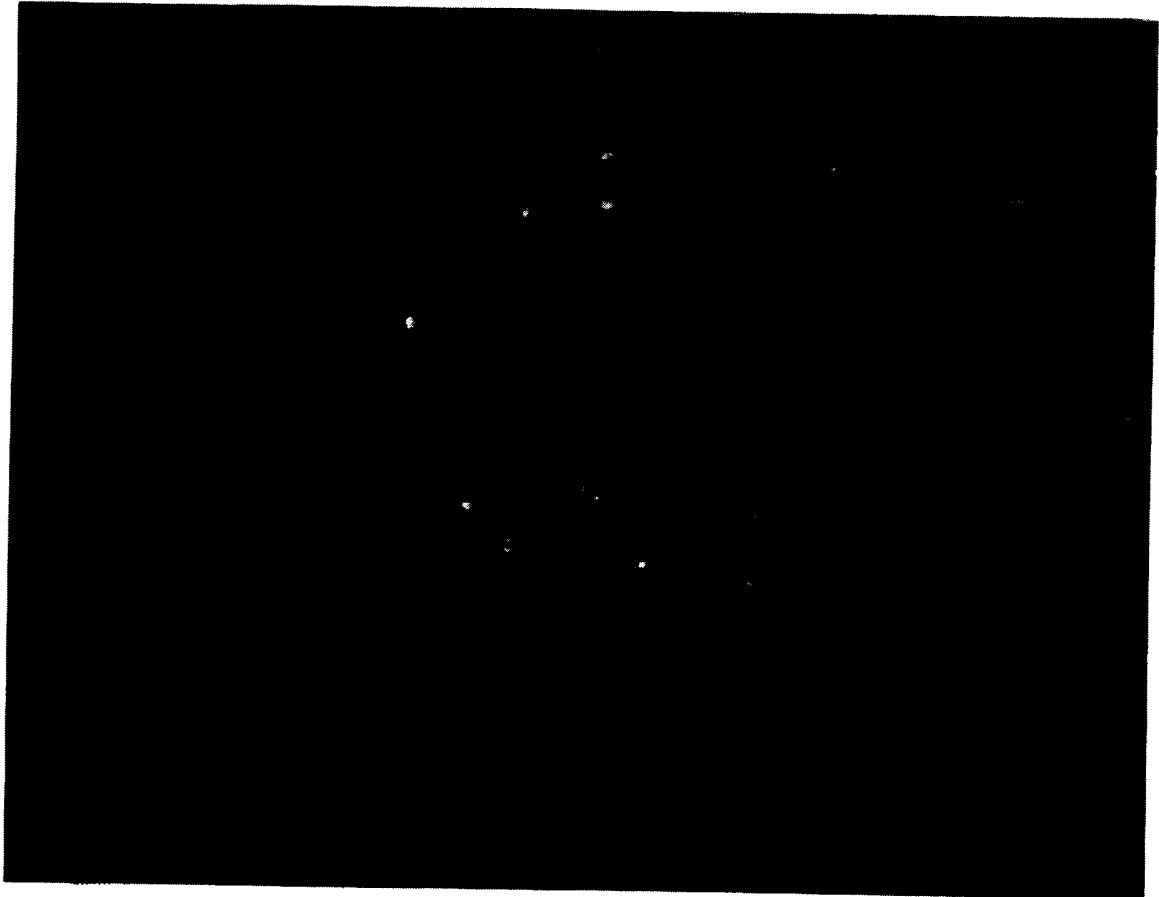


FIG.26

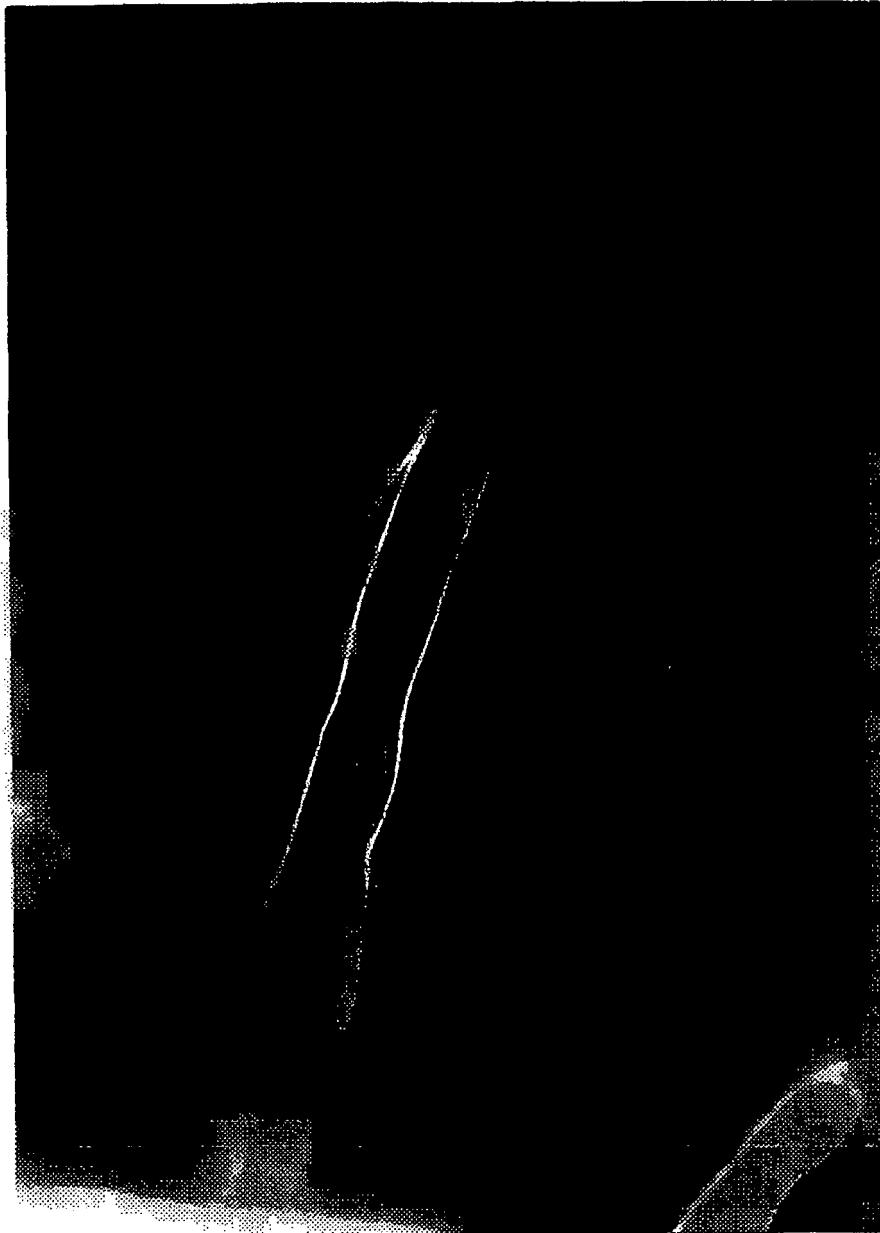


FIG.27

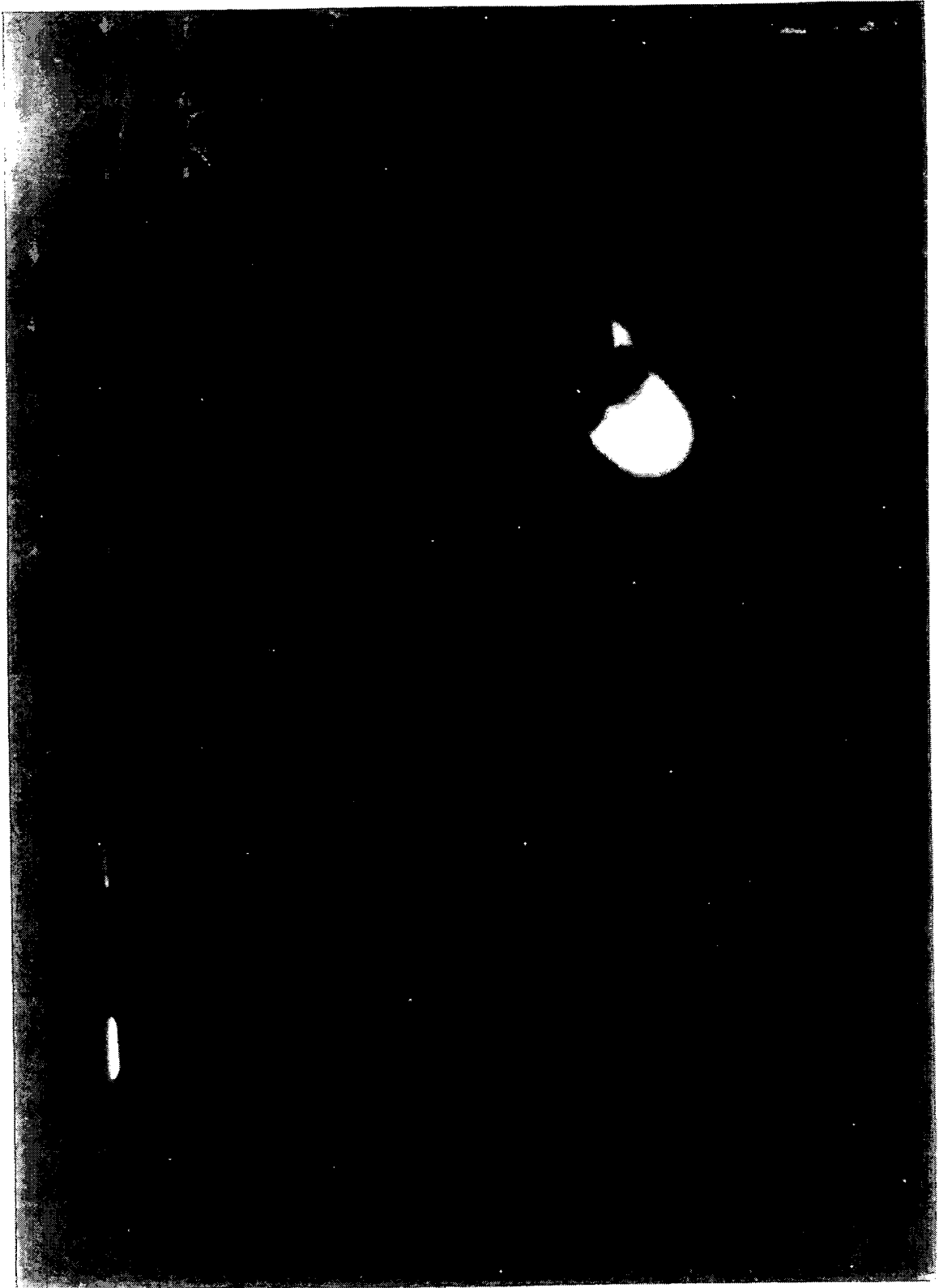


FIG. 28



FIG.29

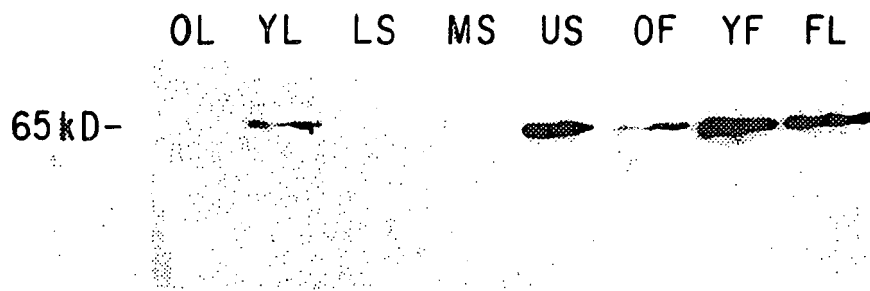


FIG.30

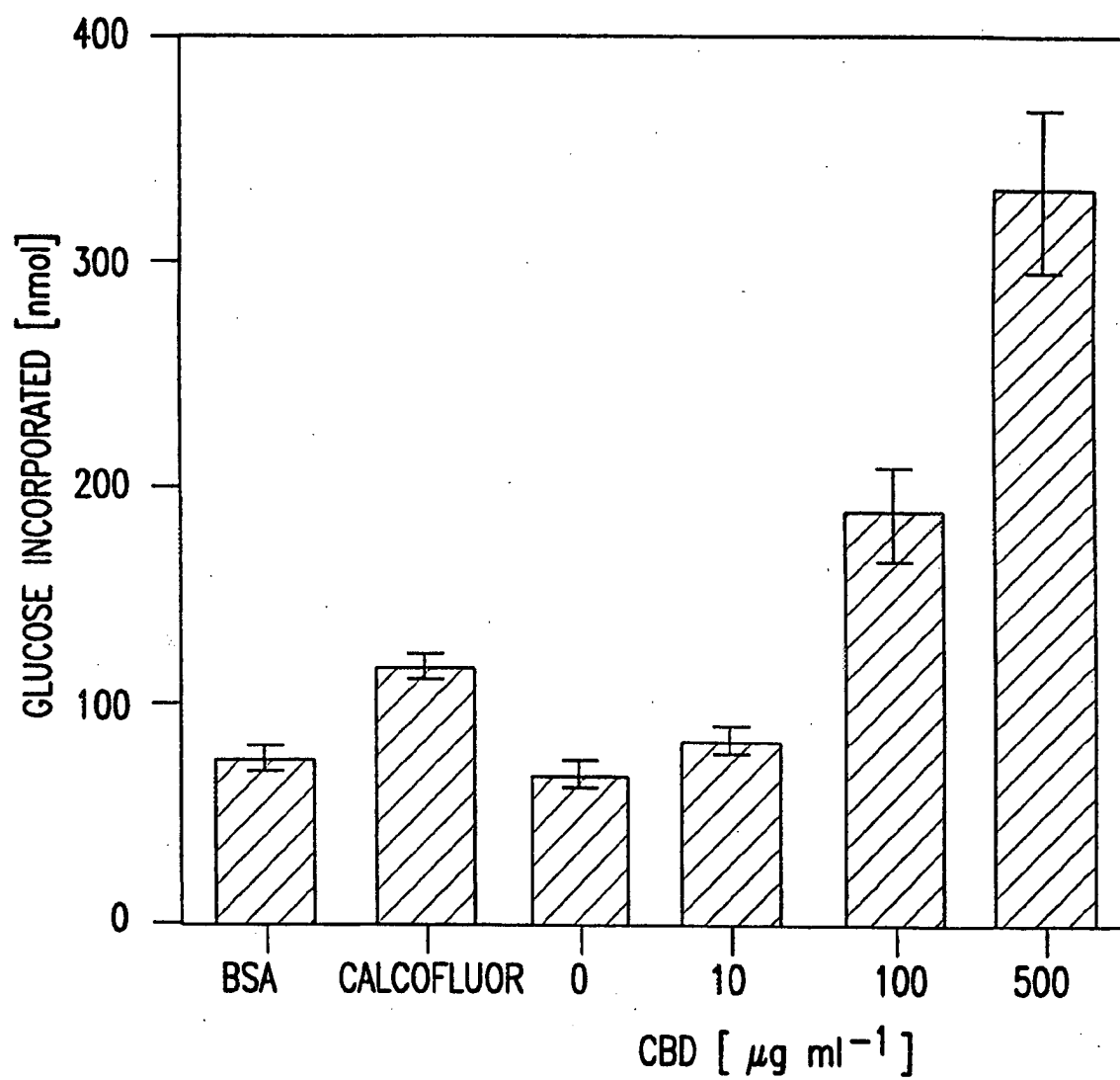


FIG.31

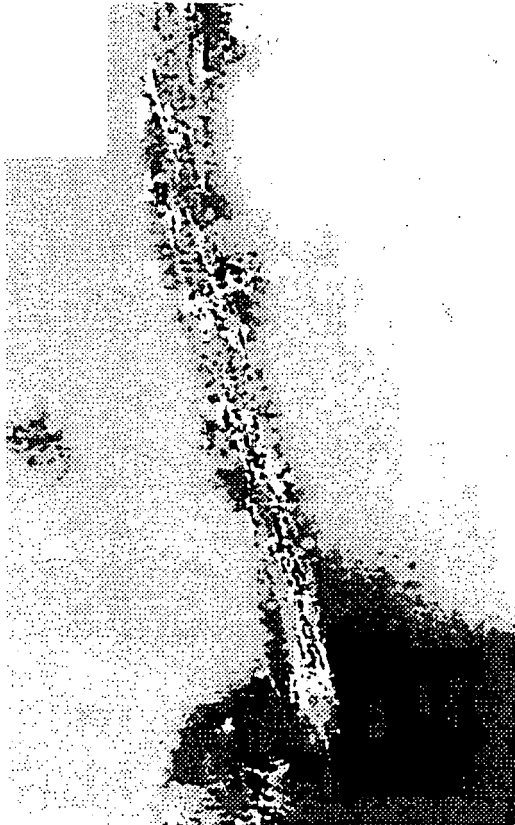


FIG. 32A



FIG. 32B

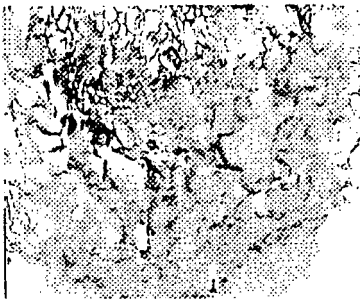


FIG. 33A



FIG. 33B



FIG. 33C



FIG. 33D



FIG. 34A

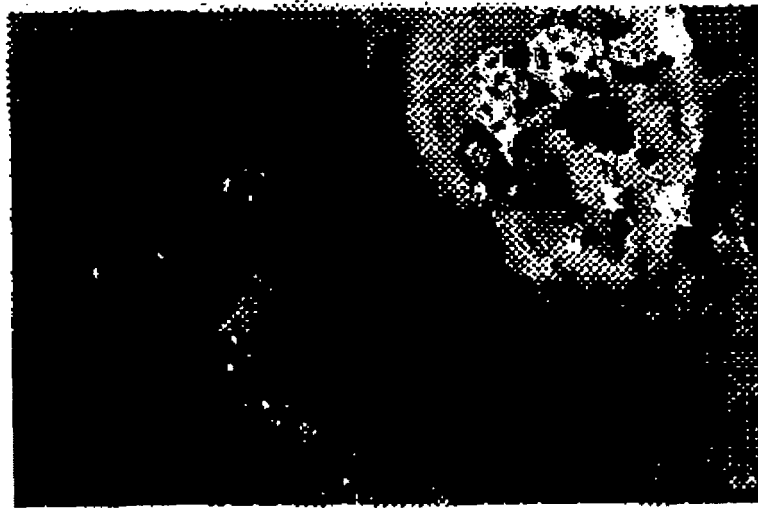


FIG. 34B

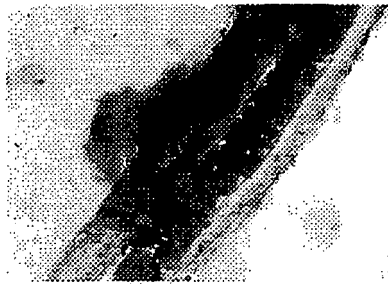


FIG.35A

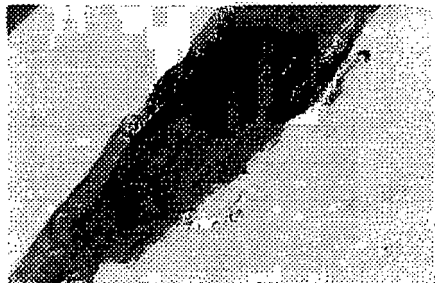


FIG.35B

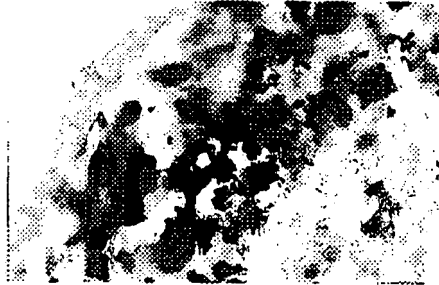


FIG.36A

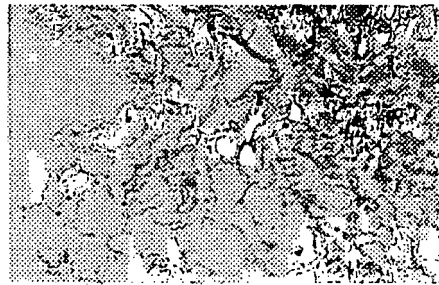


FIG.36B

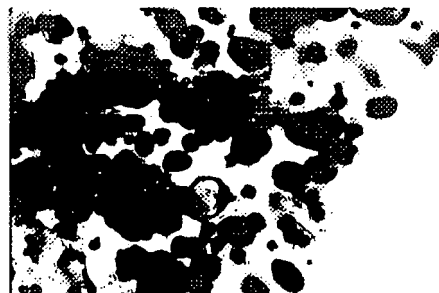


FIG.36C

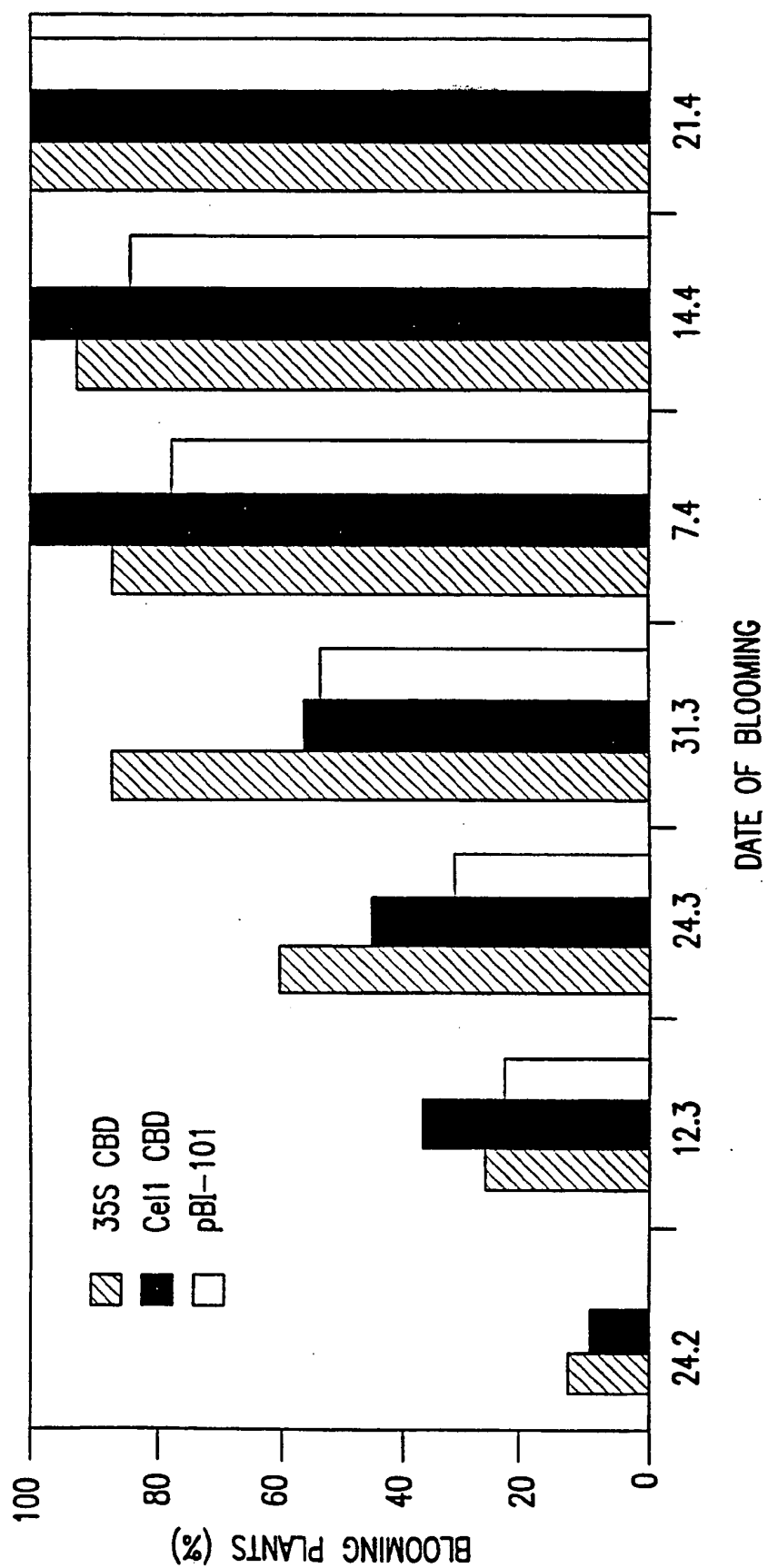


FIG.37

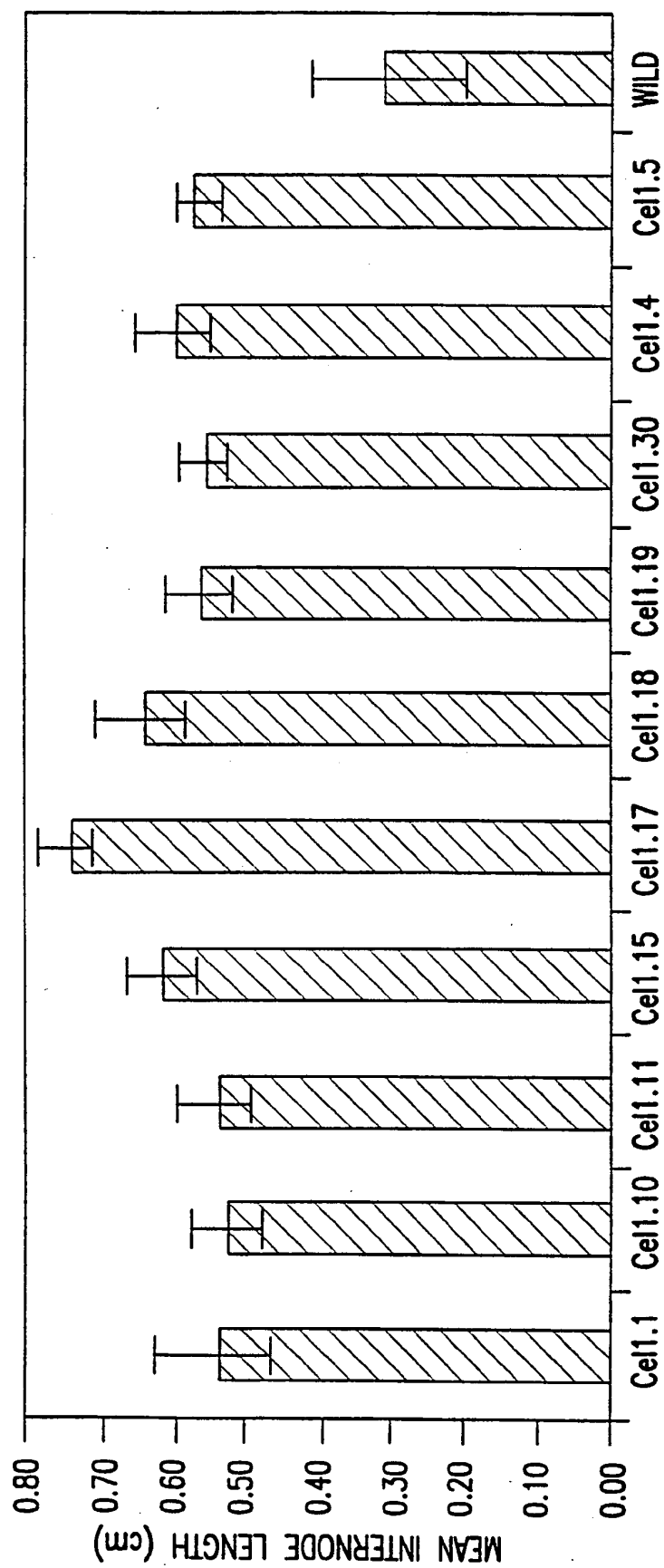


FIG.38

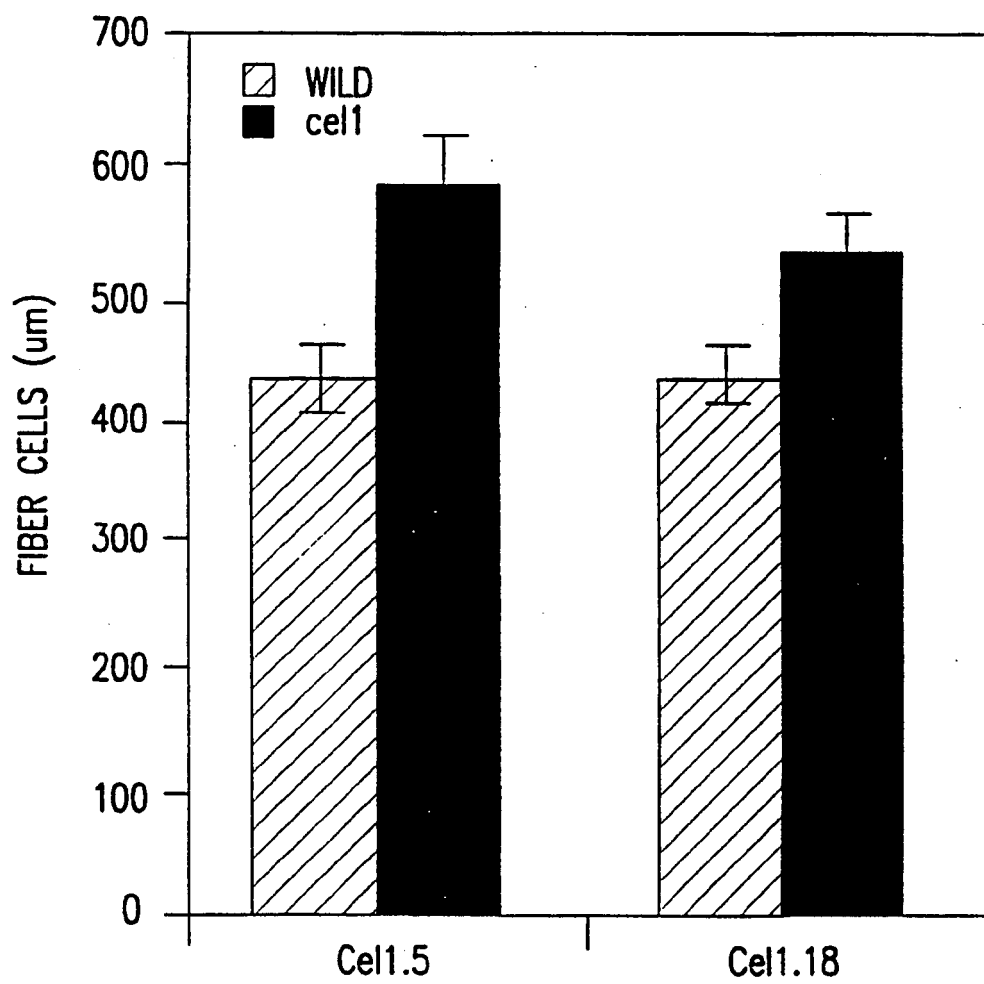


FIG.39

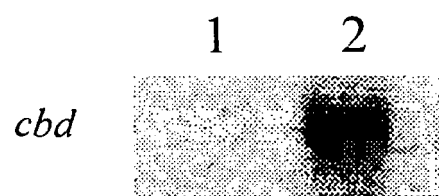


FIG.40

REFERENCES CITED IN THE DESCRIPTION

This list of references cited by the applicant is for the reader's convenience only. It does not form part of the European patent document. Even though great care has been taken in compiling the references, errors or omissions cannot be excluded and the EPO disclaims all liability in this regard.

Patent documents cited in the description

- IL 121404 [0001]
- US 006632 A [0001]
- US 09006636 B [0001]
- US 5496934 A [0019]
- WO 9424158 A [0019] [0021] [0024] [0202]
- WO 5496934 A [0183]

Non-patent literature cited in the description

- **CARPITA ; GIBEAUT.** *Plant J.*, 1993, vol. 3, 1-30 [0003] [0008]
- **COSGROVE.** *Plant Physiol.*, 1993, vol. 102, 1-6 [0003]
- **PRY.** The Growing Plant Cell Wall Chemical and Metabolic Analysis. Lonoman Scientific & Technical, 1988 [0003]
- **ROBERTS.** *Curr. Opin. Cell Biol.*, 1994, vol. 6, 688-694 [0003] [0009] [0025]
- **NISHITANI ; TOMINAGA.** *J. Biol. Chem.*, 1992, vol. 267, 21058-21064 [0003] [0025]
- **FRY et al.** *Biochem. J.*, 1992, vol. 282, 821-828 [0003] [0025]
- **MCQUEEN-MASON ; COSGROVE.** *Plant Physiol.*, 1995, vol. 107, 87-100 [0003] [0013]
- **SHOSEYOV ; DEKEL-REICHENBACH.** *Acta Hort.*, 1992, vol. 329, 225-227 [0003]
- **VERMA et al.** *J. Biol. Chem.*, 1975, vol. 250, 1019-1026 [0003]
- **HATFIELD ; NEVINS.** *Plant Physiol.*, 1987, vol. 83, 203-207 [0004]
- **HOSON ; NEVINS.** *Plant Physiol.*, 1989, vol. 90, 1353-1358 [0004] [0026]
- **INOUE ; NEVINS.** *Plant Physiol.*, 1991, vol. 96, 426-431 [0004] [0025] [0026]
- **HAYASHI.** *Ann. Rev. Plant Physiol.*, 1989, vol. 40, 139-168 [0004]
- **HAYASHI et al.** *Plant Physiol.*, 1984, vol. 25, 605-610 [0004]
- **DARVILL et al.** *Glycobiology*, 1992, vol. 2, 181-198 [0004]
- **CASS et al.** *Mol. Gen. Genet.*, 1990, vol. 223, 76-86 [0005]
- **FISCHER ; BENNETT.** *Ann. Rev. Plant Physiol. Plant Mol. Biol.*, 1991, vol. 42, 675-703 [0005]
- **LASHBROOK et al.** *Plant Cell*, 1994, vol. 6, 1485-1493 [0005] [0193]
- **TUCKER et al.** *Plant Mol. Biol.*, 1987, vol. 9, 197-203 [0005]
- **KEMMERER ; TUCKER.** *Plant Physiol.*, 1994, vol. 104, 557-562 [0005]
- **TUCKER ; MILLIGAN.** *Plant Physiol.*, 1991, vol. 95, 928-933 [0005] [0193] [0194]
- **TUCKER et al.** *Plant Physiol.*, 1988, vol. 88, 1257-1262 [0005]
- **WU et al.** *Plant Physiol.*, 1996, vol. 110, 163-170 [0006] [0193]
- *New Phytol.*, 1989, vol. 111, 323-358 [0007] [0024]
- Pollen tube emission organization and tip growth. **CRESTI ; TIEZZI.** Sexual Plant Reproduction. Springer-Verlag, 1992, 89-97 [0007]
- **HAYASHI et al.** *Plant Cell Physiol.*, 1994, vol. 35, 1199-1205 [0008]
- **FRY et al.** *Biochem J.*, 1992, vol. 282, 821-828 [0010]
- **NISHITANI ; TOMINAGA.** *J. Biol. Chem.*, 1992, vol. 267, 21058-21064 [0010]
- **MCQUEEN-MASON et al.** *Planta*, 1993, vol. 190, 327-331 [0011]
- **ALDINGTON ; FRY.** *Advances in Botanical Research*, 1993, vol. 19, 1-101 [0012]
- **YORK et al.** *Plant Physiol.*, 1984, vol. 75, 295-297 [0012]
- **MCDUGALL ; FRY.** *Planta*, 1988, vol. 175, 412-416 [0012]
- **MCDUGALL ; FRY.** *Plant Physiol.*, 1990, vol. 93, 1042-1048 [0012]
- **MCQUEEN-MASON et al.** *The Plant Cell*, 1992, vol. 4, 1425-1433 [0013] [0025]
- Relationship between polymerization and crystallization in microfibril biogenesis. **HAIGLER.** Biosynthesis and Biodegradation of Cellulose. Marcel Dekker, Inc, 1991, 99-124 [0014] [0220]
- *Planta*, 1975, vol. 126, 127-138 [0014] [0220]
- **HUGHES ; MCCULLY.** *Stain Technology*, 1975, vol. 50, 319-329 [0014]
- **HAIGLER ; BROWN.** *Science*, 1979, vol. 210, 903-906 [0014]
- **BENZIMAN et al.** *Proc. Natl. Acad. Sci.*, 1980, vol. 77, 6678-6682 [0014] [0213] [0220]
- **HAIGLER et al.** *Science*, 1980, vol. 210, 903-906 [0014] [0220]
- **BROWN et al.** *Science*, 1982, vol. 218, 1141-1142 [0014] [0220]

- **HAIGLER ; CHANZY.** *J. Ultrastruct. Mol. Struct. Res.*, 1988, vol. 98, 299-311 [0014] [0220]
- Cellulose-Binding Domains: Classification and Properties. **TOMME et al.** ACS Symposium Series 618 Enzymatic Degradation and Insoluble Carbohydrates. American Chemical society, 1995, 142-161 [0016]
- **SHOSEYOV ; DOI.** *Proc. Natl. Acad. Sci.*, 1990, vol. 87, 2192-2195 [0018]
- **SHOSEYOV et al.** *Proc. Natl. Acad. Sci.*, 1992, vol. 89, 3483-3487 [0019]
- **GOLDSTEIN et al.** *J. Bacteriol.*, 1993, vol. 175, 5762-5768 [0019] [0020] [0025]
- **MORAG et al.** *Appl. Environ. Microbiol.*, 1995, vol. 61, 1980-1986 [0020]
- Pollen tube emission, organization and tip growth. **CRESTI ; TIEZZI.** Sexual Plant Reproduction. Springer-Verlag, 1992, 89-97 [0024]
- **HAYASHI et al.** *Plant Physiol.*, 1987, vol. 83, 384-389 [0025]
- Cellulose-Binding Domains: Classification and Properties. **TOMME et al.** ACS-Symposium Series 618 Enzymatic Degradation and Insoluble Carbohydrates. American Chemical Society, 1995, 142-161 [0043]
- **TOMME et al.** *Adv. Microb. Physiol.*, 1995, vol. 37, 1 [0043]
- **SMANT et al.** *Proc. Natl. Acad. Sci.*, 1998, vol. 95, 4906-4911 [0043]
- **SMITH.** *Science*, 1985, vol. 228, 1315-1317 [0043]
- **LAM.** *Nature*, 1991, vol. 354, 82-84 [0043]
- **SAMBROOK et al.** Molecular cloning: A Laboratory Manual. Cold Spring Harbor Laboratory Press, 1989 [0067]
- **CARUTHERS et al.** *Nuc. Acids Res. Symp. Ser.*, 1980, vol. 7, 215-233 [0067]
- **CHOW ; KEMPE.** *Nuc. Acids Res.*, 1981, vol. 9, 2807-2817 [0067]
- **GELFAND.** PCR Technology, Principles and Applications for DNA Amplification. Stockton Press, 1989 [0067]
- Current Protocols In Molecular Biology. John Wiley & Sons, 1988, vol. 2 [0067]
- **SALINA et al.** *Plant Cell*, 1992, vol. 4, 1485-1493 [0070]
- **DONN et al.** *J. Mol. Appl. Genet.*, 1984, vol. 2, 549-562 [0071]
- **JEFFERSON.** *Plant Molec Biol. Rep.*, 1987, vol. 5, 387-405 [0073]
- **OW et al.** *science*, 1986, vol. 234, 856-859 [0073]
- **GOFF et al.** *EMBO J*, 1990, vol. 9, 2517-2522 [0073]
- **BEVAN.** *Nuc. Acid Res.*, 1984, vol. 12, 8711-8721 [0075]
- **HORSCH et al.** *Science*, 1985, vol. 227, 1229-1231 [0075]
- **BEVAN et al.** *Ann. Rev. Genet.*, 1982, vol. 16, 357-384 [0075]
- **ROGERS et al.** *Methods Enzymol.*, 1986, vol. 118, 627-641 [0075]
- **HERNALSTEEN et al.** *EMBO J*, 1984, vol. 3, 3039-3041 [0075]
- **HOOYKASS-VAN SLOGTEREN et al.** *Nature*, 1984, vol. 311, 763-764 [0075]
- **GRIMSLEY et al.** *Nature*, 1987, vol. 325, 1677-179 [0075]
- **BOULTON et al.** *Plant Mol. Biol.*, 1989, vol. 12, 31-40 [0075]
- **GOULD et al.** *Plant Physiol.*, 1991, vol. 95, 426-434 [0075]
- **PASZKOWSKI et al.** *EMBO J*, 1984, vol. 3, 2717-2722 [0076]
- **POTRYKUS et al.** *Molec. Gen. Genet.*, 1985, vol. 199, 169-177 [0076]
- **FROMM et al.** *Proc. Nat. Acad. Sci.*, 1985, vol. 82, 5824-5828 [0076]
- **SHIMAMOTO.** *Nature*, 1989, vol. 338, 274-276 [0076]
- **D'HALLUIN et al.** *Plant Cell*, 1992, vol. 4, 1495-1505 [0076]
- **KAEPLER et al.** *Plant Cell Reporter*, 1990, vol. 9, 415-418 [0076]
- **KLEIN et al.** *Proc. Nat. Acad. Sci.*, 1988, vol. 85, 4305-4309 [0076]
- **GORDON-KAMM et al.** *Plant Cell*, 1990, vol. 2, 603-618 [0076]
- **SHILO ; WEINBERG.** *Proc. Natl. Acad. Sci.*, 1981, vol. 78, 6789-6792 [0095]
- **SAMBROOK et al.** Molecular Cloning, A Laboratory Manual. Cold Spring Harbor Press, 1989 [0097]
- **AUSUBEL et al.** Current Protocols in Molecular Biology. Green Publishing Associates and Wiley Interscience, 1989 [0097]
- Antibodies: A Laboratory Manual. Cold Spring Harbor Press, 1988 [0107]
- **HUTCHINSON et al.** *J. Biol. Chem.*, 1978, vol. 253, 6551 [0109] [0146]
- **CREIGHTON.** Proteins: Structures and Molecular Principles. W.H. Freeman & Co, 1983 [0125]
- Oligonucleotide Synthesis. IRL Press, 1984 [0125]
- **MANIATIS et al.** Molecular Cloning A Laboratory Manual. Cold Spring Harbor Laboratory, 1989 [0130]
- **AUSUBEL et al.** Current Protocols in Molecular Biology. Greene Publishing Associates and Wiley Interscience, 1989 [0130]
- **RUTHER et al.** *EMBO J.*, 1983, vol. 2, 1791 [0133]
- **INOUE ; INOUE.** *Nucleic acids Res.*, 1985, vol. 13, 3101-3109 [0133]
- **VAN HEEKE ; SCHUSTER.** *J. Biol. Chem.*, 1989, vol. 264, 5503-5509 [0133]
- Current Protocols in Molecular Biology. Greene Publish. Assoc. & Wiley Interscience, 1988, vol. 2 [0134]
- Expression and Secretion Vectors for Yeast. **GRANT et al.** Methods in Enzymology. Acad. Press, 1987, vol. 153, 516-544 [0134]

- **GLOVER.** DNA Cloning. IRL Press, 1986, vol. II [0134]
- heterologous Gene Expression in Yeast. **BITTER.** Methods in Enzymology. Acad. Press, 1987, vol. 152, 673-684 [0134]
- The Molecular Biology of the Yeast *Saccharomyces*. Cold Spring Harbor Press, 1982, vol. I, II [0134]
- **BRISSON et al.** *Nature*, 1984, vol. 310, 511-514 [0135]
- **TAKAMATSU et al.** *EMBO J.*, 1987, vol. 6, 307-311 [0135]
- **CORUZZI et al.** *EMBO J.*, 1984, vol. 3, 1671-1680 [0135]
- **BROGLIE et al.** *Science*, 1984, vol. 224, 838-843 [0135]
- **GURLEY et al.** *Mol. Cell. Biol.*, 1986, vol. 6, 559-565 [0135]
- **WEISSBACH ; WEISSBACH.** Methods for Planet Molecular Biology. Academic Press, 1988, 421-463 [0135]
- **GRIERSON ; COREY.** Plant Molecular Biology. Blackie, 1988 [0135]
- **WIGLER et al.** *Cell*, 1997, vol. 11, 223 [0137]
- *Proc. Natl. Acad. Sci.*, 1962, vol. 48, 2026 [0137]
- **LOWY et al.** *Cell*, 1980, vol. 22, 817 [0137]
- **WIGLER et al.** *Natl. Acad. Sci.*, 1980, vol. 77, 3567 [0137]
- **O'HARE et al.** *Proc. Natl. Acad. Sci.*, 1981, vol. 78, 1527 [0137]
- **MULLIGAN ; BERG.** *Proc. Natl. Acad. Sci.*, 1981, vol. 78, 2072 [0137]
- **COLBERRE-GARAPIN et al.** *J. Mol. Biol.*, 1981, vol. 150, 1 [0137]
- **SANTERRE et al.** *Gene*, 1984, vol. 30, 147 [0137]
- **HARTMAN ; MULLIGAN.** *Proc. Natl. Acad. Sci.*, 1988, vol. 85, 8047 [0137]
- **MCCONLOQUE L.** Current Communications in Molecular Biology. Cold Spring Harbor Laboratory, 1987 [0137]
- **SCOPES.** Protein Purification: Principles and Procedure. Springer Verlag, 1987 [0139]
- **PARVEZ et al.** Progress in HPLC. Science Press, 1985, vol. 1 [0139]
- **SAMBROOK et al.** Molecular Cloning, A Laboratory Manual. Cold Spring Harbor Laboratory, 1989 [0140]
- DNA Cloning: A Practical Approach. MRL Press, Ltd, 1985, vol. I, II [0140]
- **BERNOIST ; CHAMBON.** *Nature*, 1981, vol. 290, 304-310 [0144]
- **YAMAMOTO et al.** *Cell*, 1980, vol. 22, 787-797 [0144]
- **WAGNER et al.** *Proc. Natl. Acad. Sci.*, 1981, vol. 78, 1441-1445 [0144]
- **BRINSTER et al.** *Nature*, 1982, vol. 296, 39-42 [0144]
- **VILLA-KAMAROFF et al.** *Proc. Natl. Acad. Sci.*, 1978, vol. 75, 3727-3731 [0144]
- **DEBOER et al.** *Proc. Natl. Acad. Sci.*, 1983, vol. 80, 21-25 [0144]
- Useful proteins from recombinant bacteria. Scientific American, 1980, vol. 242, 74-94 [0144]
- **HERRERA-ESTRELLA et al.** *Nature*, vol. 303, 209-213 [0144]
- **GARDNER et al.** *Nucl. Acids Res.*, 1981, vol. 9, 2871 [0144]
- **HERRERA-ESTRELLA et al.** *Nature*, 1984, vol. 310, 115-120 [0144]
- **SWIFT et al.** *cell*, 1984, vol. 38, 639-646 [0144]
- **ORNITZ et al.** Symp. Quant. Biol. Cold Spring Harbor, 1986, vol. 50, 399-409 [0144]
- **MACDONALD.** *Hepatology*, 1987, vol. 7, 425-515 [0144]
- **HANAHAN.** *Nature*, 1985, vol. 315, 115-122 [0144]
- **GROSSCHEDL et al.** *Cell*, 1984, vol. 38, 647-658 [0144]
- **ADAMES et al.** *Nature*, 1985, vol. 318, 533-538 [0144]
- **ALEXANDER et al.** *Mol. Cell. Biol.*, 1987, vol. 7, 1436-1444 [0144]
- **LEDER et al.** *Cell*, 1986, vol. 45, 485-495 [0144]
- **PINKERT et al.** *Genes and Devel.*, 1987, vol. 1, 268-276 [0144]
- **KRUMLAUF et al.** *Mol. Cell. Biol.*, 1985, vol. 5, 1639-1648 [0144]
- **HAMMER et al.** *Science*, 1987, vol. 235, 53-58 [0144]
- **KELSEY et al.** *Genes and Devel.*, 1987, vol. 1, 161-171 [0144]
- **MOGRAM et al.** *Nature*, 1985, vol. 315, 338-340 [0144]
- **KOLLIAS et al.** *Cell*, 1986, vol. 46, 89-94 [0144]
- **READHEAD et al.** *Cell*, 1987, vol. 48, 703-712 [0144]
- **SANI.** *Nature*, 1985, vol. 314, 283-286 [0144]
- **MASON et al.** *Science*, 1986, vol. 234, 1372-1378 [0144]
- **CLARK-LEWIS et al.** *Biochem.*, 1991, vol. 30, 3128-3135 [0149]
- **MERRIFIELD.** *J. Amer. Chem. Soc.*, 1963, vol. 85, 2149-2156 [0149]
- **CREIGHTON.** Proteins, Structures and Molecular Principles. W.H. Freeman and Co, 1983, 50-60 [0149]
- **CREIGHTON.** Proteins, Structures and Molecular Principles. W.H. Freeman and Co, 1983, 34-49 [0149]
- **SHIN et al.** *Biosci. Biotech. Biochem.*, 1992, vol. 56, 404-408 [0150]
- **NYFELER et al.** Peptides, Proc. 12th Amer. Pep. Soc. 1992, 661-663 [0150]
- **NOKIHARA et al.** Protein_Research Foundation. 1990, 315-320 [0150]
- **GLASS.** *Genetic Engineering News*, p., 01 October 1997, vol. 8, 41-43 [0159]
- **HENRY.** *Bull. Plant Growth Regul. Soc. Am.*, 1985, vol. 13, 9-11 [0167]

- **DOYLE ; DOYLE.** *Phytochem. Bull.*, 1987, vol. 19, 11-15 [0168]
- Degenerate primers for DNA amplification. **COMP-TON.** PCR Protocols: A Guide to Methods and Applications. Academic Press, 1990 [0169]
- Degenerate primers for DNA amplification. **COMP-TOM.** PCR Protocols: A Guide to Methods and Applications. Academic Press, 1990, 39-45 [0171]
- **SAMBROOK et al.** Molecular Cloning: A Laboratory Manual. Cold Spring Harbor Laboratory Press, 1989 [0172] [0191]
- **SOUTHERN.** *J. Mol. Biol.*, 1975, vol. 98, 503-517 [0173] [0191]
- **JEFFERSON.** *Plant Mol. Biol. Rep.*, 1987, vol. 5, 387-405 [0178]
- **AN.** *Meth. Enzymol.*, 1987, vol. 153, 292-305 [0179] [0191] [0206]
- **DEBLOCK et al.** *EMBO J.*, 1984, vol. 3, 1681 [0179] [0191]
- **JEFFERSON et al.** *Plant Mol. Biol. Rep.*, 1987, vol. 5, 387-405 [0181]
- **BROIDO et al.** *Physiologia Plantarum*, 1993, vol. 88, 259-266 [0190]
- **GUILLEY et al.** *Cell*, 1982, vol. 30, 763-773 [0190]
- **GALLIE et al.** *Nucl. Acid Res.*, 1987, vol. 15, 3257-3273 [0190]
- **TUCKER AND MILLIGAN.** *Plant Physiol.*, 1991, vol. 95, 928-933 [0193]
- **SHOSEYOV, L.** Endo-1,4- β -glucanase gene expression during adventitious root formation in Mung bean cuttings. *Master thesis, the Hebrew University of Jerusalem*, 1992 [0193]
- **LASHBROOK et al.** *The Plant Cell*, 1994, vol. 6, 1485-1493 [0194]
- **GILKES et al.** *Microbiol. Rev.*, 1991, vol. 55, 303-315 [0195]
- **HEIJNE et al.** *Eur. J. Biochem.*, 1983, vol. 133, 17-21 [0195]
- **KYTE ; DOOLITTLE.** *J. Mol. Biol.*, 1982, vol. 157, 105-132 [0197]
- **TZFIRA et al.** *Physiologia Plantarum*, 1997, vol. 99, 554-561 [0206]
- **JEFFERSON et al.** *EMBO J.*, 1987, vol. 6, 3901-3907 [0207]
- **ROSS et al.** *Microbiological Reviews*, 1991, vol. 55, 35-58 [0213]
- Relationship between polymerization and crystallization in microfibril biogenesis. **HAIGLER.** Biosynthesis and Biodegradation of cellulose. Marcel Dekker, Inc, 1991, 99-124 [0213]
- Relationship between polymerization and crystallization in microfibril biogenesis. Biosynthesis and Biodegradation of Cellulose. Marcel Dekker, Inc, 1991, 99-124 [0220]
- **HUGHES ; MCCULLY.** *EMBO J.*, 1975, vol. 6, 3901-3907 [0220]
- **HAIGLER ; BROWN.** *J. cell Biol.*, 1979, vol. 83, 70a [0220]
- **BENZIMAN et al.** *Proc. Natl. Acad. Sci.*, 1980, vol. 77, 6678-6682 [0220]